

Figure 1: 254P1D6B SSH sequence of 186 nucleotides (SEQ ID NO: 1).

```
1  GATCCACAGA TAGGACACAA TTCTTTGGTC ATCAGTAGAC CTTGAACCAT CCAAAGTAAT
61  GGAATTATTG GGAAGCACAA GAACATGTCT GCCACCAGCC CGGGCTCTGG GAGGACTATT
121 AFTTTCCTTC TTCACAGCCA CAGTGAGGGT GGACGTGCTG CTCAGTCCCT GCTGGTCTTT
181 TACTGTCAAA CGGAAGTGGT AGGTCCCCAC CTGGAGACCA GTCACAGTGG CTATTGCTTT
241 GTCAATATTT TCCATCTCCA CTGCACTGGG GCTCTGACG TGCT
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Figure 2:

Figure 2A. The cDNA (SEQ ID NO. : 2) and amino acid sequence (SEQ ID NO. : 3) of 254P1D6B v.1 clone LCP-3. The start methionine is underlined. The open reading frame extends from nucleic acid 512-3730 including the stop codon.

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1 gctgcccggggcgggtggggcgggggacccccgggggtgcaacattgctccacctgtgctgc
61 cctcggggggcctggctggccccggcgagagcggcggcggcgctcgtgtgcaactgccgga
121 ggtgagagcgcagcagtagcttcagcctgtcttgggcttggtccagattcgctcctctgg
181 ggctacgtccccggggaagaggaagcgaggattttgctgggggtggggctgtacctcttaac
241 agcaggtgcgcgcgcgagggtgtgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
301 taagacctgcgatgaacagcaggaggaacaagtgggacgycgagtgatgctcagggccag
361 cagcaacgcacatggggcgagcttcagtgctgccagcagtgaccacagttcttgaggccaaa
421 tctggctcctaaaaaacatcaaaaggaagcttgcaacccaaactctcttcagggccgcctcag
1 M A P P T G V L S S
481 aagcctgccatcacccactgtgtgtgtgtgcacaATGGCGCCCCCACAGGTGTGCTCTCTTC
11 L L L L V T I A G C A R K Q C S E G R T
541 ATTGCTGCTGCTGGTGACAATTGCAGGTTGTGCCCCGTAAGCAGTGACGAGGGGAGGAC
31 Y S N A V I S P N L E T T R I M R V S H
601 ATATTCCAATGCAGTCATTTACCTAACTTGGAAACCACCAGAATCATGCGGGTGTCTCA
51 T F P V V D C T A A C C D L S S C D L A
661 CACCTTCCCTGTCTGACTGCACGGCCGCTTGCTGTGACCTGTCCAGCTGTGACCTGGC
71 W W F E G R C Y L V S C P H K E N C E P
721 CTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCCCACAAGAGAACTGTGAGCC
91 K K M G F I R S Y L T F V L R P V Q R P
781 CAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTGCTCCGGCCTGTTCAAGAGGCC
111 A Q L L D Y G D M M L N R G S P S G I W
841 TGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGGGGCTCCCCCTCGGGGATCTG
131 G D S P E D I R K D L P F L G K D W G L
901 GGGGGACTCACTGAGGATATCAGAAAGGACTTGMCCCTTCTAGGCAAAGATTGGGGCCT
151 E E M S E Y S D D Y R E L E K D L L Q P
961 AGAGGAGATGTCTGAGTACKCAGATGACTACCGGGAGCTGGAGAAGGACCTCTTGCAACC
171 S G K Q E P R G S A E Y T D W G L L P G
1021 CAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACGGACTGGGGCCTACTGCCGGG
191 S E G A F N S S V G D S F A V P A E T Q
1081 CAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCCTGCGGTGCCAGCGGAGACGCA
211 Q D P E L H Y L N E S A S T P A P K L P
1141 GCAGGACCCTGAGCTCCATTACCTGAATGAGTCGGCTTCAACCCCTGCCCCAAACTCCC
231 E R S V L L P L P T T P S S G E V L E K
1201 TSAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCTTCAGGAGAGGTGTTGGAGAA
251 E K A S Q L Q E Q S S N S S G K E V L M
1261 AGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGCTCTGGAAAAGAGGTTCTAAT
271 P S H S L P P A S L E L S S V T V E K S

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Figure 2A-2

1321 GCCTFCCCATAGTCTTCCTCCGGCAAGCCTGGAGCTCAGCTCAGTCACCGTGGAGAAAAG
291 P V L T V T P G S T E H S I P T P P T S
1381 CCCAGTGCCTCACAGTCACCCCGGGGAGTACAGAGCACAGCATCCCAACACCTCCCACTAG
311 A A P S E S T P S E L P T S P T T A P R
1441 CGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATATCTCCTACCACTGCTCCCAG
331 T V K E L T V S A G D N L I I T L P D N
1501 GACAGTGAAAGAACTTACGGTATCGGCTGGAGATAACCTAATTATAACTTTACCCGACAA
351 E V E L K A F V A P A P P V E T T Y N Y
1561 TGAAGTTGAACTGAAGGCCTTTGTTGCGCCAGCGCCACCTGTAGAAACAACCTACAACCTA
371 E W N L I S H P T D Y Q G E I K Q G H K
1621 TGAATGGAATTTAATAAGCCACCCACAGACTACCAAGGTGAAATAAAACAAGGACACAA
391 Q T L N L S Q L S V G L Y V F K V T V S
1681 GCAAACCTCTTAACCTCTCTCAATTGTCCGTCGGACTTTATGTCTTCAAAGTCACTGTTTC
411 S E N A F G E G F V N V T V K P A R R V
1741 TAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT
431 N L P P V A V V S P Q L Q E L T L P L T
1801 CAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAAGAGCTCACTTTGCCTTTGAC
451 S A L I D G S Q S T D D T E I V S Y H W
1861 GTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACTGAAATAGTGAGTTATCATTG
471 E E I N G P F I E E K T S V D S P V L R
1921 GGAAGAAATAAACGGGCCCTTCATAGAAGAGAAGACTTCAGTTGACTCTCCCGTCTTACG
491 L S N L D P G N Y S F R L T V T D S D G
1981 CTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTGACTGTTACAGACTCGGACGG
511 A T N S T T A A L I V N N A V D Y P P V
2041 AGCCACTAACTCTACAACCTGCAGCCCTAATAGTGAACAATGCTGTGGACTACCCACCAGT
531 A N A G P N H T I T L P Q N S I T L N G
2101 TGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAAAACCTCCATCACTTTGAATGG
551 N Q S S D D H Q I V L Y E W S L G P G S
2161 AAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAGTGGTCCCTGGGTCTGGGAG
571 E G K H V V M Q G V Q T P Y L H L S A M
2221 TGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCATACCTTCATTTATCTGCAAT
591 Q E G D Y T F Q L K V T D S S R Q Q S T
2281 GCAGGAAGGAGATTATACATTTCACTGAAGGTGACAGATTCTTCAAGGCAACAGTCTAC
611 A V V T V I V Q P E N N R P P V A V A G
2341 TGCTGTRGTGACTGTGATTGTCCAGCCTGAAAACAATAGACCTCCAGTGGCTGTGGCCGG
631 P D K E L I F P V E S A T L D G S S S S
2401 CCCTGATAAAGAGCTGATCTTCCAGTGGAAAGTGCTACCCCTGGATGGGAGCAGCAGCAG
651 D D H G I V F Y H W E H V R G P S A V E
2461 CGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTCAGAGGCCCCAGTGCAGTGGGA
671 M E N I D K A I A T V T G L Q V G T Y H
2521 GATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGTCTCCAGGTGGGGACCTACCA

Figure 2A-3

691 F R L T V K D Q Q G L S S T S T L T V A
2581 CTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGCACGTCCACCCTCACTGTGGC
711 V K K E N N S P P R A R A G G R S V L V
2641 TGTGAAGAAGGAAAATAATAGTCCTCCAGAGCCCGGGCTGGTGGCAGACATGTTCTTGT
731 L P N N S I T L D G S R S T D D Q R I V
2701 GCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCTACTGATGACCAAAGAATTGT
751 S Y L W I R D G Q S P A A G D V I D G S
2761 GTCCTATCTGTGGATCCGGGATGCCAGAGTCCAGCAGCTGGAGATGTCATCGATGGCTC
771 D H S V A L Q L T N L V E G V Y T F H L
2821 TGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAGGGGGTGTACACTTTCCACTT
791 R V T D S Q G A S D T D T A T V E V Q P
2881 GCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACTGCCACTGTGGAAGTGCAGCC
811 D P R K S G L V E L T L Q V G V G Q L T
2941 AGACCCTAGGAAGAGTGGCCTGCTGGAGCTGACCCCTGCAGGTTGGTGTGGGCAGCTGAC
831 E Q R K D T L V R Q L A V L L N V L D S
3001 AGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTGCTGCTGAACGTGCTGGACTC
351 D I K V Q K I R A H S D L S T V I V F Y
3061 GGACATTAAGGTCCAGAAGATTGGGGCCCACTCGGATCTCAGCACCGTGATTGTGTTTTA
871 V Q S R P P F K V L K A A E V A R N L H
3121 TGTACAGAGCAGGCCCGCCTTTCAAGGTTCTCAAAGCTGCTGAAGTGGCCCCGAAATCTGCA
891 M R L S K E K A D F L L F K V L R V D T
3181 CATCGGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTCAAGGTTCTGAGGGTTGATAC
911 A G C L L K C S G H G H C D P L T K R C
3241 AGCAGGTTGCCTTCTGAAGTGTCTGGCCATGGTCACTGCGACCCCTCACAAAGCGCTG
931 I C S H L W M E N L I Q R Y I W D G E S
3301 CATTTGCTCTCACTTATGGATGAGAACCTTATACAGCSTTATATCTGGGATGGAGAGAG
951 N C E W S I F Y V T V L A F T L I V L T
3361 CAACTGTGAGTGGAGTATATTCTATGTGACAGTGTGGCTTTTACTCTTATTGTGCTAAC
971 G G F T W L C I C C C K R Q K R T K I R
3421 AGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGACAAAAAGGACTAAAATCAG
991 K K T K Y T I L D N M D E Q E R M E L R
3481 GAAAAAACAAGTACACCATCCTGGATAACATGGATGAACAGGAAAGAATGGAAGTGA
1011 P K Y G I K H R S T E H N S S L M V S E
3541 GCCCAAATATGGTATCAAGCACCGAAGCACAGAGCACAACTCCAGCCTGATGGTATCCGA
1031 S E F D S D Q D T I F S R E K M E R G N
3601 GTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGAGAAAAGATGGAGAGAGGGAA
1051 P K V S M N G S I R N G A S F S Y C S K
3661 TCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCTTCTTCAGTTATTGCTCAAA
1071 D R *
3721 GGACAGATAAtggcgagtttcattgttaaagtgggaaggacccyttgaatccargaccagtc
3781 agtgggagttacagcacaaaacccactcttttagaatagttcattgaccttcttccccag

Figure 2A-4

3841 tgggttagatgtgtatccccacgtactaaaaagaccgggtttttgaaggcacaaaaacaaaaa
3901 ctttgctcttttaactgagatgcttggttaatagaaataaaggctgggtaaaaactytaagg
3961 tatatacttaaaagagttttgagttttttagctggcacaaatctcatattaaagatgaac
4021 aacgatttcttatctgtagaacotttagagaagggtgaatgaaacaagggttttaaaaaagggat
4081 gattttctgtcttagcgtgtgtgattgcctctaaaggaacagcattctaaacacgggtttctc
4141 ttgtaggacctgcagtcagatggctgtgtatgtttaaaatagcttgtctaaagaggcaccggg
4201 ccactctgtggaggtacggaggtcttgcatgttagcaagctttctgtgctgaaggcaaacctc
4261 gcacagtgcacagccctcctgggttttaattctgtgctatgtcaatggcagttttcatct
4321 ctctcaagaaagcagctgttggccattcaagagctaagggaagaatcgtattctaaaggaact
4381 gaggcaatagaaaggggaggaggagcttaatgccttgagggtgaaggtagcattgtaac
4441 attatcttttctttcttaagaaaaactacactgactcctctcgggtgtttgttttagcagta
4501 tagttctctaatgtaaacrgatccccagttttacatttaartgcaatagaagtgttaattc
4561 attaaagcattttattatgttctgttaggtgtgctgttggactgccatagataggkataacg
4621 actcagcaattgtgttatattccaaaaactctgaaatacagtcagtccttaacttggatgg
4681 cgtgggttatgatactctgggtccccgacagggtactttccaaaataacttgacatagatgta
4741 ttcacttcataatgtttaaaaatacatttaagtttttctaccgaataaatctttatttcaaa
4801 catgaaagacaattaaaaacattccccccccacaaagcagtaactcccgagcaatttaactgga
4861 gttaattgttagcctgctacgtttgactgggttcagggttagttcccatccacccttggctct
4921 gaggctgggtggccttgggtgggtgcocttggcattttttgtgggaagattagaatgagagat
4981 agaaccagtggtgtggtaccaagtgtgagcacacctaaacaatatcctgttgcacaatgc
5041 ttttttaacacatgggaaaaactaggaatgcattgctgatgaagaagcaagggtattttaaac
5101 accagggcaggagtgccagagaaaaatgtttcccatgggttcttaaaaaaaattcagott
5161 ttaggtgcttttgtcatctcccgagttatcctcctcatgggaccatcttatttttactt
5221 attgtaatttactggggaaaaggcagaactaaaaagtgtgtcatttttatttttaaaataat
5281 tgctttgcttatgctacactttctgtataactagccaattcaatactgtctatagtgtt
5341 agaaggaaaatgtgatttttttttttaaccagttattgagcttcataagcctagaatctg
5401 ccttatcaggtgaccaggggttatggttggttgcatgcaaatgtgaattttctggcataggg
5461 gacagcagocaaaatgtaaagtcatogggcgtaatgaggaagaaggaggtgaacattttac
5521 cgctttakgtacataacatattgcagtttaacatactcatttgatccttataatcaaccttg
5581 aagaggagatactatcattcttatgttgccagatagccctctgaaggcccagagaggttaa
5641 rtaacttcccagaggtcatggocaaagaagttagtggctccaagaactgaatgcaaattttt
5701 taaactgtagagttctgctttccactaaacaaagaactcctgccttgatggatggagggc
5761 aaattctggtggaacttttggggccacctgaaagtcttatccaggactaagaggaattt
5821 cttttaatggatccagagagccaaaggctcagaggagagatggcctgcatagtctcctgtg
5881 gatcacacccggggccacccctccctctagggtttacagtggacttctctgccccctcctcc
5941 tttctgtccttggccatctcagcctggcctctctgatccttccatcacagaaggatctt
6001 gaatctctgggaaatcaaacatcacagtagtgatcagaaagtgaagtcctgtcttgcacc
6061 ccattttctcatcagaacaaagcaccgagatggaatgaccaaccagcattcttcatgggtgga
6121 ctgcttatcattgaggatctttgggagataaaagcacgctaagagctctggacagagaaaa
6181 acaggccctagaatatgggagtggtgtttgtagggtctcayargctaacaagcacttttag
6241 ttgctgggtttacattcaatgaaggaggattcatacccatggcattacaaggctaagcatg

Figure 2A-5

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6301 tgtatgactaaggaactatctgaaaaacatgcagcaaggtaagaaaatgtaccactcaac
6361 aagccagtgatgccaccttttgtgcgcggggaggagagtgactaccattgttttttgtgt
6421 gacaaagctatcatggactattttaattcttggttttattgcttaaaatataattttttc
6481 cctatgtgttgacaaggatatttctaataatcacactatttaaatatataactaataaat
6541 aaagggtgtctgtattttctgtaattgttttttagggggaaatttgttttctttatgct
6601 tcagggttagagggattcccttgagtataggtcagcacaactctggcctgcagcctgtgtgt
6661 gcacgccccatgagcogaaaagtgggtcttatgttttcaaatgggttaaaaaataaataaaa
6721 aaatttgaaacatgtgaactatatgacattcagatttgtgttcaataaataaagttttatt
6781 ggaacatatcc

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Figure 2B. The cDNA (SEQ ID NO. : 4) and amino acid sequence (SEQ ID NO. : 5) of 254P1D6B v.2.

The start methionine is underlined. The open reading frame extends from nucleic acid 512-3730 including the stop codon.

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1 gctgcgcggggcggtggggcggggatcccccggggtgcaaccttgctccacctgtgtctgc
61 cctcgggcggtggtggtggccccgcgcagagcgggcgggcgctcgctgtcactgccgga
121 ggtgagagcgcagcagtagcttcagcctgtcttggtggtccagattcgctcctctgg
181 ggctacgtccccgggaagaggaagcgaggattttgctgggggtggggctgtacctctaac
241 agcaggtgcgcgcgaggggtgtgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
301 taagacctgcgatgacgacgaggaggaacaagtgggacggcgagtgatgctcagggccag
361 cagcaacgcattggggcgagcttcagtgctgcgcagcagtgaccacagttcttgaggccaaa
421 tctggctcctaaaaaacatcaaaaggaagcttgcaccaaactctcttcaggggccgcctcag
1 M A P P T G V L S S
481 aagcctgccatcacccactgtgtggtgcacaATGGCGCCCCCACAGGTGTGCTCTCTTC
11 L L L L V T I A G C A R K Q C S E G R T
541 ATTGCTGCTGCTGGTGACAATTGCAGGTTGTGCCCCGTAAGCAGTGCGAGCGAGGGGAGGAC
31 Y S N A V I S F N L E T T R I M R V S H
601 ATATTCGAATGCAGTCATTTCACCTAACTTGGAAACACCAGAAATCATGCGGGTGTCTCA
51 T F P V V D C T A A C C D L S S C D L A
661 CACCTTCCCTGTCTGACTGCACGGCCGCTTGCTGTGACCTGTCCAGCTGTGACCTGGC
71 W W F E G R C Y L V S C P H K E N C E P
721 CTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCCCACAAAGAGAACTGTGAGCC
91 K K M G F I R S Y L T F V L R F V Q R P
781 CAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTGCTCCGGCCCTGTTTCAGAGGCC
111 A Q L L D Y G D M M L N R G S P S G I W
841 TGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGGGGCTCCCCCTCGGGGATCTG
131 G D S P E D I R K D L P F L G K D W G L
901 GGGGGAATCACCTGAGGATATCAGAAAGGACTTGCCTTTCTAGGCAAGATTGGGGCCT
151 E E M S E Y A D D Y R E L E K D L L Q P
961 AGAGGAGATGTCTGAGTACGCAGATGACTACCGGGAGCTGGAGAAGGACCTCTTGCAACC
171 S G K Q E P R G S A E Y T D W G L L P G
1021 CASTGGCAAGCAGGAGCCCAGAGGGAGTCCCGAGTACACGGACTGGGGCCTACTGCCGGG

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Figure 2B-2

191 S E G A F N S S V G D S P A V P A E T Q
1081 CAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCCTGCGGTGCCAGCGGAGACGCA
211 Q D F E L S Y L N E S A S T P A F K L P
1141 GCAGGACCCTGAGCTCCATTACCTGAATGAGTCGGCTTCAACCCCTGCCCCAAAACCTCCC
231 E R S V L L F L P T T P S S G E V L E K
1201 TGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCTTCAGGAGAGGTGTTGGAGAA
251 E K A S Q L Q E Q S S N S S G K E V L M
1261 AGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGCTCTGGAAAAGAGGTTCTAAT
271 P S H S L F P A S L E L S S V T V E K S
1321 GCCTTCCCATAGTCTTCCCTCCGGCAAGCCTGGAGCTCAGCTCAGTCACCGTGGAGAAAAG
291 P V L T V T P G S T E H S I P T P P T S
1381 CCCAGTGCCTCAGCTCACCCCGGGGAGTACAGAGCACAGCATCCCAACACCTCCCCTACTAG
311 A A P S E S T P S E L P I S P T T A P R
1441 CGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATATCTCCTACCCTGCTCCCAG
331 T V K E L T V S A G D N L I I T L P D N
1501 GACAGTGAAAGAACTTACGGTATCGGCTGGAGATAACCTAATTATAACTTTACCCGACAA
351 E V E L K A F V A P A P P V E T T Y N Y
1561 TGAAGTTGAAGTGAAGGCCTTTGTTGCGCCAGCGCCACCTGTAGAAACAACCTACAACATA
371 E W N L I S H P T D Y Q G E I K Q G H K
1621 TGAATGGAATTTAATAAGCCACCCACAGACTACCAAGGTGAAATAAAACAAGGACACAA
391 Q T L N L S Q L S V G L Y V F K V T V S
1681 GCAAACCTCTTAACCTCTCTCAATTGTCCGTCGGACTTTATGTCTTCAAAGTCACTGTTTC
411 S E N A F G E G F V N V T V K P A R R V
1741 TAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT
431 N L P F V A V V S P Q L Q E L T L P L T
1801 CAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAAGAGCTCACTTTGCCTTTGAC
451 S A L I D G S Q S T D D T E I V S Y H W
1861 GTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACTGAAATAGTGAGTTATCATTG
471 E E I N G P F I E E K T S V D S P V L R
1921 GGAAGAAATAAACGGGCCCTTCATAGAAGAGAAGACTTCAGTTGACTCTCCCGTCTTACG
491 L S N L D P G N Y S F R L T V T D S D G
1981 CTTGTCTAACCTTGATCCTGGTAACATAGTTTCAGGTTGACTGTACAGACTCGGACGG
511 A T N S T T A A L I V N N A V D Y P P V
2041 AGCCACTAAGTCTACAAGTGCAGCCCTAATAGTGAACAATGCTGTGGACTACCCACCACT
531 A N A G P N H T I T L P Q N S I T L N G
2101 TGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAAAACCTCCATCACTTTGAATGG
551 N Q S S D D H Q I V L Y E W S L G F G S
2161 AAACCAGAGCAGTGACGATCACCAGATTGTCTCTATGAGTGGTCCCTGGGTCTGGGAG
571 E G K H V V M Q G V Q T F Y L H L S A M
2221 TGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCATACCTTCATTTATCTGCAAT
591 Q E G D Y T F Q L K V T D S S R Q Q S T

Figure 2B-3

2281 GCAGGAAGGAGATTATACATTTTCAGCTGAAGGTGACAGATTCTTCAAGGCAACAGTCTAC
611 A V V T V I V Q P E N N R P P V A V A G
2341 TGCTGTAGTGAAGTGTGATTGTCCAGCCTGAAAAACAATAGACCTCCAGTGGCTGTGGCCGG
631 P D K E L I F P V E S A T L D G S S S S
2401 CCCTGATAAAGAGCTGATCTTCCCAGTGGAAAGTGCTACCCCTGGATGGGAGCAGCAGCAG
651 D D H G I V F Y H W E H V R G P S A V E
2461 CGATGACCACGGCATTGTCTTCTACCACTGGGAGCAGCTCAGAGGCCCCAGTGCAGTGGGA
671 M E N I D K A I A T V T G L Q V G T Y H
2521 GATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGTCTCCAGGTGGGGACCTACCA
691 F R L T V K D Q Q G L S S T S T L T V A
2581 CTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGCAGCTCCACCCCTCACTGTGGC
711 V K K E N N S P P R A R A G G R H V L V
2641 TGTGAAGAAGGAAAATAATAGTCCTCCAGAGCCCCGGGCTGGTGGCAGACATGTTCTTGT
731 L P N N S I T L D G S R S T D D Q R I V
2701 GCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCTACTGATGACCAAAGAATTGT
751 S Y L W I R D G Q S P A A G D V I D G S
2761 GTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCTGGAGATGTCATCGATGGCTC
771 D H S V A L Q L T N L V E G V Y T F H L
2821 TGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAGGGGGTGTACACTTTCCACTT
791 R V T D S Q G A S D T D T A T V E V Q P
2881 GCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACTGCCACTGTGGAAGTGCAGCC
811 D P R K S G L V E L T L Q V G V G Q L T
2941 AGACCCCTAGGAAGAGTGGCCTGGTGGAGCTGACCCTGCAGGTTGGTGTGGGCAGCTGAC
831 E Q R K D T L V R Q L A V L L N V L D S
3001 AGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTGCTGCTGAACGTGCTGGACTC
851 D I K V Q K I R A H S D L S T V I V F Y
3061 GGACATTAAGGTCCAGAAGATTCCGGCCCCACTCGGATCTCAGCACCGTGATTGTGTTTTA
871 V Q S R P P F K V L K A A E V A R N L H
3121 TGTACAGAGCAGGCCCGCCTTTCAAGGTTCTCAAAGCTGCTGAAGTGGCCCCGAAATCTGCA
391 M R L S K E K A D F L L F K V L R V D T
3181 CATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTCAAGGTCTTGAGGGTTGATAC
911 A G C L L K C S G H G H C D P L T K R C
3241 AGCAGGTTGCCTTCTGAAGTGTCTGGCCATGGTCACTGCGACCCCTCACAAAGCGCTG
931 I C S H L W M E N L I Q R Y I W D G E S
3301 CATTGCTCTCACTTATGGATGGAGAACCCTTATACAGCGTTATATCTGGGATGGAGAGAG
951 N C E W S I F Y V T V L A F T L I V L T
3361 CAACTGTGAGTGGAGTATATTCTATGTGACAGTGTGGCTTTTACTCTTATTGTGCTAAC
971 G G F T W L C I C C C K R Q K R T K I R
3421 AGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGACAAAAAAGGACTAAAATCAG
991 K K T K Y T I L D N M D E Q E R M E L R
3481 GAAAAAACAAGTACACCATCCTGGATAACATGGATGAACAGGAAAGAATGGAAGTGAAG

Figure 2B-4

1011 P K Y G I R H R S T E H N S S L M V S E
3541 GCCCAAATATGGTATCAAGCACCGAAGCACAGAGCCAACTCCAGCCTGATGGTATCCGA
1031 S E F D S D Q D T I F S R E K M E R G N
3601 GTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGAGAAAAGATGGAGAGAGGGAA
1051 P K V S M N G S I R N G A S F S Y C S K
3661 TCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCTTCCTTCAGTTATTGCTCAAA
1071 D R *
3721 GGACAGATAAtggcgaggttcattgttaaagtggagggaccccttgaatccaagaccagtc
3781 agtgggaggttacagcacaaaaacccactcttttagaatagttcattgaccttcttcccccag
3841 tgggttagatgtgtatccccacgtactaaaagaccgggtttttgaaggcacaaaaacaaaaa
3901 ctttgctcttttaactgagatgcttgttaabagaaataaaggctgggtaaaaactctaagg
3961 tatatacttaaaagagttttgagttttttagtctggcacaatctcatattaaagatgaac
4021 aacgattttctatctgtagaacotttagagaaggtgaatgaaacaagggttttaaaaaagggat
4081 gatttctgtcttagccgctgtgattgcctctaaaggaacagcattctaaacacgggtttctc
4141 ttgtaggacctgcagtcagatggctgtgtatgttbaaaatagcttgtctaagaggcaccggg
4201 ccactctgtggaggtacggagtccttgcagtgtagcaagctttctgtgctgacggcacaactc
4261 gcacagtgccaagccctcctgggtttttaattctgtgctatgtcaatggcagttttcatct
4321 ctctcaagaaagcagctgttgccattcaagagctaagggaagaatcgtattctaaggact
4381 gaggcaatagaaaaggggaggaggagcttaatgccgtgcaggttgaaggtagcattgtaac
4441 attatcttttctttctctaagaaaaactacactgactcctctcgggtgttgttttagcagta
4501 tagttctctaattgtaaacggatccccagttttacattaaatgcaatagaagtgttaattc
4561 attaaagcatttattatgttctgtaggctgtgcgttttggaactgccatagatagggataaag
4621 actcagcaattgtgtatatattccaaaactctgaaatacagtcagtccttaacttggatgg
4681 cgtgggttatgatactctgggtcccccagaggtactttccaaaataacttgacatagatgta
4741 ttcaacttcatatgtttaaaaatacatttaagtttttctaacgaataaaatcttattttcaaa
4801 catgaaagacaattaaaaacattcccacccacaaaagcagtcactcccgagcaattaaactgga
4861 gtttaattgtagcctgctacgttgaactgggttcagggtagttcccatccaccccttggctct
4921 gaggtctgggtggttgggtggtggttggcattttttgtgggaagattagaatgagagat
4981 agaaccagtggttgggtaccaagtgtgagcacacctaacaataatcctgttgcaaatgc
5041 ttttttaacacatgggaaaaactaggaatgcattgctgatgaagaagcaagggtatttaaac
5101 accaggggcaggagtgccagagaaaaatgtttcccatgggttcttaaaaaaaattcagctt
5161 ttaggtgcttttgtcatctcccgaggtatttcactcctcatgggaccatcttatttttactt
5221 attgtaatttactggggaaaaggcagaactaaaaagtggtgtcattttatttttaaaataat
5281 tgctttgcttatgcctacactttctgtataactagccaattcaatactgtctatagtgtt
5341 agaaggaaaatgtgatttttttttttaaccagtbattgagcttcataagcctagaatctg
5401 ccttatcaggtgaccaggggttatgggtgtttgcatgcaaatgtgaatttctggcataggg
5461 gacagcagcccaaatgtaaaagtcacgggogtaatgaggaagaaggaggagtgaacatttac
5521 cgctttatgtacataacatattgcagtttacatactcatttgatccttataatcaaccttg
5581 aagaggagatactatcattccttatgttgcagatagccctctgaaggcccagagaggttaa
5641 gtaacttcccagaggtcatggccaagaagtagtggtctccaagaactgaatgcaattttt
5701 taaactgtagagttctgctttccactaaacaaagaactcctgccttgatggatggagggc

Figure 2B-5

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5761 aaattctgggtggaacttttggggccacctgaaagtcttatccaggactaagaggaattt
5821 cttttaatggatccagagagccaagggtcagagggagagatggcctgcatagtctcctgtg
5881 gatcacacccggggccacccctccctctaggtttacagtggacttcttctgcccctccctcc
5941 tttctgtctcttggccatctcagcctggcctctctgatccctccatccagaaggatctt
6001 gaatctctgggaaatcaaacatcacagtagtgatcagaaagtgagtccctgtcttgtcacc
6061 ccatttctcatcagaacaaagcacagagatggaatgaccaaccagcattcttcatgggtgga
6121 cggcttatcattgaggatctttgggagataaagcacgctaagagctctggacagagaaaa
6181 acaggccctagaatatgggagtggtgtttgttagggctcataggctaacaagcacttttag
6241 ttgctgggtttacattcaatgaaggaggattcatacccatggcattacaaggctaagcatg
6301 tgtatgactaaggaactatctgaaaaacatgcagcaaggtaagaaaatgtaccactcaac
6361 aagccagtgatgccaccttttgtgcgcggggaggagagtgactaccattgttttttgtgt
6421 gacaaagctatcatggactattttaattcttgggttttattgcttaaaatatattatttttc
6481 cctatgtgttgacaagggtatttctaataatcacactattaaatatatgcactaatctaaat
6541 aaaggtgtctgtatttttctgtaatgcttatttttagggggaaatttgttttctttatgct
6601 tcagggttagagggattcccttgagtatagggtcagcaaacctctggcctgcagcctgtgtgt
6661 gcacgccccatgagccgaaaagtgggtcttatgttttcaaatgggttaaaaaataaataaaa
6721 aaatttgaaacatgtgaactatatgacattoagatttgrgttcataaataaagttttatt
6781 ggaacatatcc

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Figure 2C. The cDNA (SEQ ID NO. : 6) and amino acid sequence (SEQ ID NO. : 7) of 254P1D6B v.3.

The start methionine is underlined. The open reading frame extends from nucleic acid 739-3930 including the stop codon.

```

1 gctgccgcgggcgggtggggcggggatcccccggggggtgcaaccttgctccacctgtgtgtgc
61 cctcgggcgggcctgggtggcccccgcgcagagcggcgggcggtcgtcgtgtcactgccggga
121 ggtgagagcgcagcagtagcttcagcctgtcttgggcttgggtccagattcgctcctctgg
181 ggctacgtcccggggaagaggaagcgcaggattttgctgggggtggggctgtacctottaac
241 agcagggtgcgcgcgcgcaggggtgtgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
301 taagacctgcgatgaagcgcagggaggaacaagtgggacggcgagtgatgctcagggccag
361 cagcaacgcctggggcgagcttcagtgtgcgcagcagtgaccacaggtacgggtatctact
421 tcccagagcgccctggccgagaaataggaaagagggcagccagtaggcaggccaataccca
481 acaaaagtagaatcgagacgccttgagttcagaagttcttgaggccaaatctggctccta
541 aaaaacatcaaaggaagcttgcaaaaaactctcttcagggccgcctcagaagcctgccat
601 caccactgtgtggtgcacaatggcgccccccacaggtgtgtgtctctcttcattgtgtgtgc
661 tgggtgacaattgcagtttgcattatgggtggatgcactcatggcaaaaaaatcactgggtgag
1 M T R L G W P S P C C A R K
721 catcatttaagaagacccATGACTAGACTGGGCTGGCCGAGCCCATGTTGTGCCCGTAAG
15 Q C S E G R T Y S N A V I S P N L E T T
781 CAGTGCAGCGAGGGGAGGACATATTTCCAATGCAGTCATTTCACCTAACTTGGAAACCACC
35 R I M P V S H T F F V V D C T A A C C D
841 AGAATCATGCGGGTGTCTCACACCTTCCCTGTCTGCTAGACTGCACGGCCGCTTGTCTGTGAC
55 L S S C D L A W W F E G R C Y L V S C P

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Figure 2C-2

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901 CTGTCCAGCTGTGACCTGGCCTGGTGGTTTCGAGGGGCGCTGCTACCTGGTGAGCTGCCCC
75 H K E N C E P K K M G P I R S Y L T F V
961 CACAAAGAGAACTGTGAGCCCAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTG
95 L R P V Q R P A Q L L D Y G D M M L N R
1021 CTCCGGCCTGTTTCAGAGGCCTGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGG
115 G S P S G I W G D S P E D I R K D L P F
1081 GGCTCCCCCTCGGGGATCTGGGGGGACTCACCTGAGGATATCAGAAAGGACTTGCCCTTT
135 L G K D W G L E E M S E Y S D D Y R E L
1141 CTAGGCAAAGATTGGGGCCTAGAGGAGATGTCTGAGTACTCAGATGACTACCGGGGAGCTG
155 E K D L L Q P S G K Q E P R G S A E Y T
1201 GAGAAGGACCTCTTGCAACCCAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACG
175 D W G L L P G S E G A F N S S V G D S P
1261 GACTGGGGCCTACTGCCGGGCAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCTCT
195 A V P A E T Q Q D P E L H Y L N E S A S
1321 GCGGTGCCAGCGGAGACGCAGCAGGACCTGAGCTOCATTACCTGAATGAGTCGGCTTCA
215 T P A P K L P E R S V L L P L P T T P S
1381 ACCCCTGCCCCAAAACCTCCCTGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCT
235 S G E V L E K E K A S Q L Q E Q S S N S
1441 TCAGGAGAGGTGTTGGAGAAAAGAAAAGCCTTCTCAGCTCCAGGAACAATCCAGCAACAGC
255 S G K E V L M P S H S L P P A S L E L S
1501 TCTGGAAAAGAGGTTCTAATGCCTTCCCATAGTCTTCCCTCCGGCAAGCCTGGAGCTCAGC
275 S V T V E K S P V L T V T P G S T E H S
1561 TCASTCACCGTGGAGAAAAGCCCAGTGCCTCACAGTCACCCCGGGGAGTACAGAGCACAGC
295 I P T P P T S A A P S E S T P S E L P I
1621 ATCCCAACACCTCCCCTAGCGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATA
315 S P T T A P R T V K E L T V S A G D N L
1681 TCTCCTACCACTGCTCCCAGGACAGTGAAAGAACTTACGSTATCGGCTGGAGATAACCTA
335 I I T L P D N E V E L K A F V A P A P P
1741 ATTATAACTTTACCCGACAATGAAGTTGAACTGAAGGCCTTTGTTGCGCCAGCGCCACCT
355 V E T T Y N Y E W N L I S H P T D Y Q G
1801 GTAGAAACAACCTACAACCTATGAATGGAATTTAATAAGCCACCCACAGACTACCAAGGT
375 E I K Q G H K Q T L N L S Q L S V G L Y
1861 GAAATAAAACAAGGACACAAGCAAACCTCTTAACCTCTCTCAATTGTCCGTGGGACTTTAT
395 V F K V T V S S E N A F G E G F V N V T
1921 GTCTTCAAAGTCACTGTTTCTAGTGAAAACGCCCTTTGGAGAAGGATTTGTCAATGTCACCT
415 V K P A P R V N L P P V A V V S P Q L Q
1981 GTTAAGCCTGCCAGAAGAGTCAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAA
435 E L T L P L T S A L I D G S Q S T D D T
2041 GAGCTCACTTTGCCTTTTGACGTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACT
455 E I V S Y H W E E I N G P F I E E K T S
2101 GAAATAGTGAGTTATCATTGGGAAGAAATAAACGGGCCCCCTCATAGAAGAGAAGACTTCA
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Figure 2C-3

475 V D S P V L R L S N L D P G N Y S F R L
2161 GTTGACTCTCCCGTCTTACGCTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTG
495 T V T D S D G A T N S T T A A L I V N N
2221 ACTGTTACAGACTCGGACGGAGCCACTAACTCTACAAGTGCAGCCCTAATAGTGAACAAT
515 A V D Y P P V A N A G P N H T I T L P Q
2281 GCTGTGGACTACCCACCAGTTGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAA
535 N S I T L N G N Q S S D D H Q I V L Y E
2341 AACTCCATCACTTTGAATGGAAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAG
555 W S L G P G S E G K H V V M Q G V Q T F
2401 TGGTCCCTGGGTCCTGGGAGTGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCA
575 Y L H L S A M Q E G D Y T F Q L K V T D
2461 TACCTTCATTTATCTGCAATGCAGGAAGGAGATTATACATTTTCAGCTGAAGGTGACAGAT
595 S S R Q Q S T A V V T V I V Q P E N N R
2521 TCTTCAAGGCAACAGTCTACTGCTGTGGTGACTGTGATTGTCCAGCCTGAAAACAATAGA
615 F P V A V A G P D K E L I F P V E S A T
2581 CCTCCAGTGGCTGTGGCCGGCCCTGATAAAGAGCTGATCTTCCAGTGGAAAGTGCTACC
635 L D G S S S S D D H G I V F Y H W E H V
2641 CTGGATGGGAGCAGCAGCAGCGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTC
655 R G P S A V E M E N I D K A I A T V T G
2701 AGAGGCCCCAGTGCAGTGGAGATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGT
675 L Q V G T Y H F R L T V K D Q Q G L S S
2761 CTCCAGGTGGGACCTACCACTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGC
695 T S T L T V A V K K E N N S P P R A R A
2821 ACGTCCACCCTCACTGTGGCTGTGAAGAAGGAAAATAATAGTCCTCCAGAGCCCGGGCT
715 G G R H V L V L P N N S I T L D G S R S
2881 GGTGGCAGACATGTTCTTGTGCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCT
735 T D D Q R I V S Y L W I R D G Q S P A A
2941 ACTGATGACCAAAGAATTGTGTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCT
755 G D V I D G S D H S V A L Q L T N L V E
3001 GGAGATGTCATCGATGGCTCTGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAG
775 G V Y T F H L R V T D S Q G A S D T D T
3061 GGGGTGTACACTTTCCACTTCCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACT
795 A T V E V Q P D P R K S G L V E L T L Q
3121 GCCACTGTGGAAGTGCAGCCAGACCCTAGGAAGAGTGGCCTGGTGGAGCTGACCCTGCAG
815 V G V G Q L T E Q R K D T L V R Q L A V
3181 GTTGGTGTGGGAGCTGACAGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTG
835 L L N V L D S D I K V Q K I R A H S D L
3241 CTGCTGAACGTGCTGGACTCGGACATTAAGGTCCAGAAGATTCGGGCCCCACTCGGATCTC
855 S T V I V F Y V Q S R P P F K V L K A A
3301 AGCACCGTGATTGTGTTTTATGTACAGAGCAGGCCGCCCTTTCAAGGTTCTCAAAGCTGCT
875 E V A R N L H M R L S K E K A D F L L F

Figure 2C-4

3361 GAAGTGGCCCGAAATCTGCACATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTC
895 K V L R V D T A G C L L K C S G H G H C
3421 AAGSTCFTGAGGGTTGATACAGCAGGTTGCCFTCTGAAGTGTCTGGCCATGGTCACTGC
915 D F L T K R C I C S H L W M E N L I Q R
3481 GACCCCTCACAAGCGCTGCATTTGCTCTCACTTATGGATGGAGAACCTTATACAGCGT
935 Y I W D G E S N C E W S I F Y V T V L A
3541 TATATCTGGGATGGAGAGAGCAACTGTGAGTGGAGTATATCTATGTGACAGTGTGGCT
955 F T L I V L T G G F T W L C I C C C K R
3601 TTTACTCTTATTGTGCTAACAGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGA
975 Q K R T K I R K K T K Y T I L D N M D E
3661 CAAAAAGGACTAAAATCAGGAAAAAACAAGTACACCATCCTGGATAACATGGATGAA
995 Q E R M E L R P K Y G I K H R S T E H N
3721 CAGGAAAGAATGGAAGTGGAGGCCCCAAATATGGTATCAAGCACCAGCAGAGCACAAC
1015 S S L M V S E S E F D S D Q D T I F S R
3781 TCCAGCCTGATGGTATCCGAGTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGA
1035 E K M E R G N P K V S M N G S I R N G A
3841 GAAAAGATGGAGAGAGGGAATCCAAAGGTTTCCATGAATGGTCCATCAGAAATGGAGCT
1055 S F S Y C S K D R *
3901 TCCTTCAGTTATTGCTCAAAGGACAGATAAatggcgagttcattgttaaagtggaaggacc
3961 ccttgaatccaagaccagtcagtgagggttacagcacaaaaccactcttttagaatagt
4021 tcattgaccttcttccccagtgagggttagatgtgtatccccacgtactaaaagaccggttt
4081 ttgaaggcacaaaaacaaaaactttgtcttttaactgagatgcttgttaatatagaaataaa
4141 ggctgggtaaaactctaaggtatataacttaaaagagttttgagttttttagctggcaca
4201 atctcatattaaagatgaacaacgattttctatctgtagaaccttagagaaggtgaatgaa
4261 acaagggttttaaaaagggtgattttctgtcttagccgtgtgattgctctaagggaacag
4321 cattctaacaacgggtttctctttagtagacctgcagtcagatggctgtgtatgttaaaata
4381 gcttgtctaagaggcacgggcatctgtggaggtacggagtccttgcatgtagcaagcttt
4441 ctgtgctgaaggcaacaactgcacagtgccaagcctcctgggttttaattctgtgtat
4501 gtcaatggcagttttcatctctctcaagaaagcagctgttggccattcaagagctaagga
4561 agaatcgtattctaaggactgaggcaatagaaaggggaggaggagcttaatgccgtgcag
4621 gttgaaggtagcattgttaacattatcttttcttcttaagaaaaactacactgaactct
4681 ctcggtgttgttttagcagtabagttctctaagttaaocggatccccagtttacattaat
4741 gcaatagaagtgattaattcattaagcatttattatgttctgtaggctgtgcgtttggac
4801 tgccatagatagggataaacgactcagcaattgtgtatatattccaaaactctgaaataca
4861 gtcagtccttaacttggtatggcgtggttatgatactctgggtcccgacaggtactttccaa
4921 aataacttgacatagatgtattcacttcatatgttttaaaaatacatttaagttttttctac
4981 cgaataaatcttattttcaaacatgaaagacaattaaaacattcccacccacaaagcagta
5041 ctcccgagcaattaaactggagtttaattgttagcctgctacgttgactgggttcagggttagtt
5101 ccccatccacccttggtcctgaggctgggtggccttggtgggtgcccttggcattttttgtg
5161 ggaagattagaatgagagatagaaccagtggtgtgtgtaccgaagtgtgagcacacctaacc
5221 aatatcctgttgcacaatgcttttttaacacatgggaaaactaggaatgcattgctgatg

Figure 2C-5

5281 aagaagcaagggtattttaaacaccagggcaggagtgccagagaaaatgtttcccccattgggt
5341 tcttaaaaaaaattcagcttttaggtgcttttgctcatctcccgaggtattcactcctcatg
5401 ggaccatcttatttttaacttattgttaatttactggggaaaggcagaactaaaaagtgtgt
5461 ctttttattttttaaaataatttgctttgcttatgctctacactttctgtataactagccaat
5521 tcaatactgtctatagtgttagaaggaaaaatgtgatttttttttttaaccagtattgag
5581 cttcataagccctagaatctgcttatcagggtgaccaggggttatgggtgtttgcatgcaaa
5641 tgtgaattttctggcataggggacagcagcccaaatgtaaagtcacgggogtaattgagga
5701 agaaggagtgaaacatttaccgctttatgtacataacatattgcagtttacatactcattt
5761 gatccttataatcaacottgaaggaggagatactatcattcttatgtttgcagatagccctc
5821 tgaaggcccagagaggttaagtaacttcccagaggtcatggccaagaagtagtggtcca
5881 agaactgaatgcaaaattttttaaactgtagagttctgctttccactaaacaaagaactcc
5941 tgctttgatggatggaggggcaaatctctggtggaaacttttggggccacctgaaagttctatt
6001 cccaggactaagaggaattttcttttaattggatccagagagccaaggtcagagggagagat
6061 ggcttgcatagtctcctgtggatcacacccggggccacccctccctctaggtttacagtgg
6121 acttcttctgcccctcctcctttttctgtccttgggcatctcagcctggcctctctgatcc
6181 ttccatcacagaaggatcttgaatctctgggaaatcaaacatcacagtagtgatcagaaa
6241 gtgagtcctgtcttgctcaccocattttctcatcagaacaaagcacgagatggaatgaccaa
6301 ccagcattcttcatgggtggaactgcttatcattgaggatctttgggagataaaagcacgcta
6361 agagctctggacagagaaaaaacaggccctagaatatgggagtggtgtttgtagggctca
6421 taggctaacaagcacttttagttgctggtttacattcaatgaaggaggattcatacccatg
6481 gcattacaaggctaagcatgtgtatgactaaggaaactatctgaaaaacatgcagcaaggt
6541 aagaaaatgtaccactcaacaagccagtgatgccaccttttgtgcgcggggaggagagtg
6601 actaccattgttttttgtgtgacaaagctatcatggactatttttaactcttggttttattg
6661 cttaaaatatattatttttccctatgtgttgacaaaggtattttctaatatcacactattaa
6721 atatatgcactaatctaaataaaagggtgtctgtattttctgtaatgcttatttttaggggg
6781 aaatttgttttctttatgcttcagggttagagggattcccttgagtataggtcagcaact
6841 ctggcctgcagcctgtgtgtgcacgccccatgagccgaaaagtgggtcttatgttttcaa
6901 atggttaaaaataaaataaaaaaatttgaaacatgtgaaactatatgacattcagattttgtg
6961 ttcataaataaagttttatttgaacatatcc

Figure 2D. 254P1D6B v.4 through v.20, SNP variants of 254P1D6B v.1. The 254P1D6B v.4 through v.20 proteins have 1072 amino acids. Variants 254P1D6B v.4 through v.20 are variants with single nucleotide difference from 254P1D6B v.1. 254P1D6B v.5 and v.6 proteins differ from 254P1D6B v.1 by one amino acid. 254P1D6B v.4 and v.7 through v.20 proteins code for the same protein as v.1. Though these SNP variants are shown separately, they can also occur in any combinations and in any of the transcript variants listed above in Figures 2A, Figure 2B and Figure 2C.

Variant	Nucleic acid position	Nucleic Acid Variation	Amino Acid Position	Amino Acid Variation
254P1D6B v.4	286	C/G	<i>Silent variant</i>	
254P1D6B v.5	935	C/A	142	P=>T
254P1D6B v.6 (Identical AA as v.2)	980	T/G	157	S=>A
254P1D6B v.7	2347	G/A	<i>Silent variant</i>	
254P1D6B v.8	3762	C/T	<i>Silent variant</i>	
254P1D6B v.9	3772	A/G	<i>Silent variant</i>	
254P1D6B v.10	3955	C/T	<i>Silent variant</i>	
254P1D6B v.11	4096	C/T	<i>Silent variant</i>	
254P1D6B v.12	4415	G/A	<i>Silent variant</i>	
254P1D6B v.13	4519	G/A	<i>Silent variant</i>	
254P1D6B v.14	4539	A/G	<i>Silent variant</i>	
254P1D6B v.15	4614	G/T	<i>Silent variant</i>	
254P1D6B v.16	5184	G/C	<i>Silent variant</i>	
254P1D6B v.17	5528	T/G	<i>Silent variant</i>	
254P1D6B v.18	5641	G/A	<i>Silent variant</i>	
254P1D6B v.19	6221	T/C	<i>Silent variant</i>	
254P1D6B v.20	6223	G/A	<i>Silent variant</i>	

Figure 3:

Figure 3A. Amino acid sequence 254P1D6B v.1 clone LCP-3 (SEQ ID NO. : 8). The 254P1D6B v.1 clone LCP-3 protein has 1072 amino acids.

```

1  MAPPTGVLSS  LLLLVTIAGC  ARKQCSEGR  YSNAVISP  ETTRIMRV  TFPVVDCTAA
61  CCDLSSCDLA  WWFEGRCYL  SCPHKENCE  KKMGPIRS  TFVLRPVQ  AQLLDYGDMM
121 LNRGSPSGIW  GDSPEDIRK  LPFLGKDW  EEMSEYS  RELEKDLL  SGKQEPGSA
181 EYTDWGLLP  SEGAFNSSV  DSPAVPAET  QDPELHYL  SASTPAPK  ERSVLLPLPT
241 TPSSGEVLE  EKASQLQEQ  SNSSGKEV  PSHSLPPA  ELSSVTVE  PVLTVTPGST
301 EHSIPTPPT  AAPSESTP  LPISPTTAP  TVKELTVS  DNLIITLP  EVELKAFVAP
361 APPVETTYN  EWNLI SHPTD  YQGEIKQG  QTLNLSQL  GLYVFKVT  SENAFGEGFV
421 NVTVKPARR  NLPPVAVVS  QLQELTLP  SALIDGSQ  DDEIVSYH  EEINGPFIEE
481 KTSVDSPLR  LSNLDPGNY  FRLTVTDS  ATNSTTAA  VNNAVDYP  ANAGPNHTIT
541 LPQNSITLN  NQSSDDHQ  LYEWSLGP  EGKHVVMQ  QTPYLHLS  QEGDYTFQLK
601 VTDSSRQQS  AVTVIVQPE  NNRPPVAV  PDKELIFV  SATLDGSS  DDHGIVFYHW
661 EHVRGPSAV  MENIDKAI  VTGLQVG  FRLTVKDQ  LSSTSTLT  VKKENNSPFR
721 ARAGGRHVL  LPNNSITLD  SRSTDDQR  SYLWIRDG  PAAGDVID  DHSVALQLTN
781 LVEGVYTFH  RVTDSQGA  TDTATVEV  DPRKSGLV  TLQVGVGQ  EQRKDTLVRQ
841 LAVLLNVLD  DIKVQKIR  SDLSTVIV  VQSRPPEK  KAAEVARN  MRLSKEKADF
901 LLFKVLRVD  AGCLLKCS  GHCDPLTK  ICSHLWM  IQRYIWDG  NCEWSIFYVT
961 VLAFTLIV  GGFTWLCI  CKRQKR  KTKYTILD  MDEQERM  PKYGIKHRST
1021 EHNSSLMV  SEFDSQDT  FSREKMER  PKVSMNGS  NGASFYS  DR

```

Figure 3B. Amino acid sequence 254P1D6B v.2 (SEQ ID NO.: 9). The 254P1D6B v.2 protein has 1072 amino acids.

```

1  MAPPTGVLSS  LLLLVTIAGC  ARKQCSEGR  YSNAVISP  ETTRIMRV  TFPVVDCTAA
61  CCDLSSCDLA  WWFEGRCYL  SCPHKENCE  KKMGPIRS  TFVLRPVQ  AQLLDYGDMM
121 LNRGSPSGIW  GDSPEDIRK  LPFLGKDW  EEMSEYAD  RELEKDLL  SGKQEPGSA
181 EYTDWGLLP  SEGAFNSSV  DSPAVPAET  QDPELHYL  SASTPAPK  ERSVLLPLPT
241 TPSSGEVLE  EKASQLQEQ  SNSSGKEV  PSHSLPPA  ELSSVTVE  PVLTVTPGST
301 EHSIPTPPT  AAPSESTP  LPISPTTAP  TVKELTVS  DNLIITLP  EVELKAFVAP
361 APPVETTYN  EWNLI SHPTD  YQGEIKQG  QTLNLSQL  GLYVFKVT  SENAFGEGFV
421 NVTVKPARR  NLPPVAVVS  QLQELTLP  SALIDGSQ  DDEIVSYH  EEINGPFIEE
481 KTSVDSPLR  LSNLDPGNY  FRLTVTDS  ATNSTTAA  VNNAVDYP  ANAGPNHTIT
541 LPQNSITLN  NQSSDDHQ  LYEWSLGP  EGKHVVMQ  QTPYLHLS  QEGDYTFQLK
601 VTDSSRQQS  AVTVIVQPE  NNRPPVAV  PDKELIFV  SATLDGSS  DDHGIVFYHW
661 EHVRGPSAV  MENIDKAI  VTGLQVG  FRLTVKDQ  LSSTSTLT  VKKENNSPFR
721 ARAGGRHVL  LPNNSITLD  SRSTDDQR  SYLWIRDG  PAAGDVID  DHSVALQLTN
781 LVEGVYTFH  RVTDSQGA  TDTATVEV  DPRKSGLV  TLQVGVGQ  EQRKDTLVRQ
841 LAVLLNVLD  DIKVQKIR  SDLSTVIV  VQSRPPEK  KAAEVARN  MRLSKEKADF
901 LLFKVLRVD  AGCLLKCS  GHCDPLTK  ICSHLWM  IQRYIWDG  NCEWSIFYVT

```


Figure 3B-2

961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSQDQTI FSREKMERGN PKVSMNGSIR NGASFYSYCSK DR

Figure 3C. Amino acid sequence 254P1D6B v.3 (SEQ ID NO: 10). The 254P1D6B v.3 protein has 1063 amino acids.

1 MTRLGWSPSPC CARKQCSEGR TYSNAVISPN LETTRIMRVS HTFPVVDCTA ACCDLSSCDL
61 ANWFEGRCYL VSCPHKENCE PKKMGPIRSY LTFVLRPVQR PAQLLDYGDM MLNRGSPSGI
121 WGDSPEDIRK DLPFLGKDWG LEEMSEYSDD YRELEKDLLQ PSGKQEPGRS AEYTDWGLLP
181 GSEGAFNSSV GDSPAVPAET QQDPPELHYLN ESASTPAPKL PERSVLLPLP TTPSSGEVLE
241 KEKASQLQEQ SSNSSGKEVL MPSSSLPPAS LELSSVTVEK SPVLTVTTPGS TEHSIPTPTT
301 SAAPSESTPS ELPISPTTAP RTVKELTVSA GDNLIITLFD NEVELKAFVA PAPPVETTYN
361 YEWNLISHPT DYQGEIKQGH KQTLNLSQLS VGLYVFKVTV SSENAFGEGF VNVTVKPARR
421 VNLPPVAVVS PQLQELTLPL TSALIDGSQS TDDTEIVSYH WEEINGPFIE EKTSVDSFVL
481 PLSNLDPGNY SFRLTVTDSG GATNSTTAAL IVNNAVDPYP VANAGPNHTI TLPQNSITLN
541 GNQSSDDHQI VLYEWSLPGS SEGKHVVMQG VQTPYLHLSA MQEGDYTFQL KVTDSRQQS
601 TAVVTIVVQP ENNRPPVAVA GPDKELIFFV ESATLDGSSS SDDHGIVFYH WEHVRGPSAV
661 EMENIDKAIAT TVTGLQVGTY HFRLTVKDQQ GLSSTSTLTV AVKKENNSPP RARAGGRHVL
721 VLPNNSITLD GSRSTDDQRI VSYLWIRDGQ SPAAGDVIDG SDHSVALQLT NLVEGVYTFH
781 LRVTDSQGAS DTDATVEVQ PDPKSGLVE LTLQVGVGQL TEQRKDTLVR QLAVLLNVLD
941 SDIKVQKIRA HSDLSTVIVF YVQSRPPFKV LKAAEVARNL HMRLSKEKAD FLLFKVLRVD
901 TAGCLLKCSG HGHCDELTKR CICSLLWMEN LIQRYIWDGE SNCEWSIFYV TVLAFTLIVL
961 TGGFTWLCIC CCKRQKRTKI RKKTKYTILD NMDEQERMEL RPKYGIKHS TEHNSSLMVS
1021 ESEFDSQDQI FFSREKMERG NPKVSMNGSI RNASFYSYCS KDR

Figure 3D. Amino acid sequence 254P1D6B v.5 (SEQ ID NO: 11). The 254P1D6B v.5 protein has 1072 amino acids.

1 MAPPTGVLSS LLLLVTIAGC ARKQCSEGRY TYSNAVISPNL ETTRIMRVSH TFPVVDCTAA
61 CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPISYLV TFLVRPVQRP AQLLDYGDM
121 LNRGSPSGIW GDSPEDIRKD LTFGLGKDWGL EEMSEYSDDY RELEKDLLQP SGKQEPGRSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPPELHYLNE SASTPAPKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
301 EHSIPTPTTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLFDN EVELKAFVAP
361 APPVETTYNY EWNLIHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDEIVSYHW EEINGPFIEE
481 KTSVDSFVLR LSNLDPGNYS FRLTVTDSG ATNSTTAALI VNNNAVDPYPV ANAGPNHTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLPGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQGST AVVTIVVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
661 EHVRGPSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPKSGLVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDL DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADF

Figure 3D-2

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901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSQDQTI FSREKMEPGN PKVSMNGSIR NGASFYSYCSK DR

```

Figure 3E. Amino acid sequence 254P1D6B v.6 (SEQ ID NO: 12). The 254P1D6B v.6 protein has 1072 amino acids.

```

1 MAPFTGVLSS LLLLVTIAGC ARKQCSEGRF YSNAVITSPNL ETTRIMRVSH TFPVVDCTAA
61 CCCLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPFRSYL TFVLRPVQRP AQLLDYGDMM
121 INRGSPSGIW GDSPEDIRKD LPFLGKDWGL EEMSEYADDY RELEKDLLQP SGKQEFGRSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPHELHYLN SASTPAKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLFPASL ELSSVTVEKS PVLTVPFGST
301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLDPN EVELKAFVAP
361 APPVETTYNY EWNLIHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDEIVSYHW EEINGPFTEE
481 KTSVDSFVLR LSNLDPGNYS FRLTVTDSOG ATNSTTAALI VNNAVDPFV ANAGPNHTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLGPGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQQST AVVTIVVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
661 EHVRGFSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYFFHL RVTDSQGASD TDTATVEVQP DPRKSGLEVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLB MRLSKEKADF
901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSQDQTI FSREKMERGN PKVSMNGSIR NGASFYSYCSK DR

```

Figure 4: Expression of 254P1D6b in 293T cells

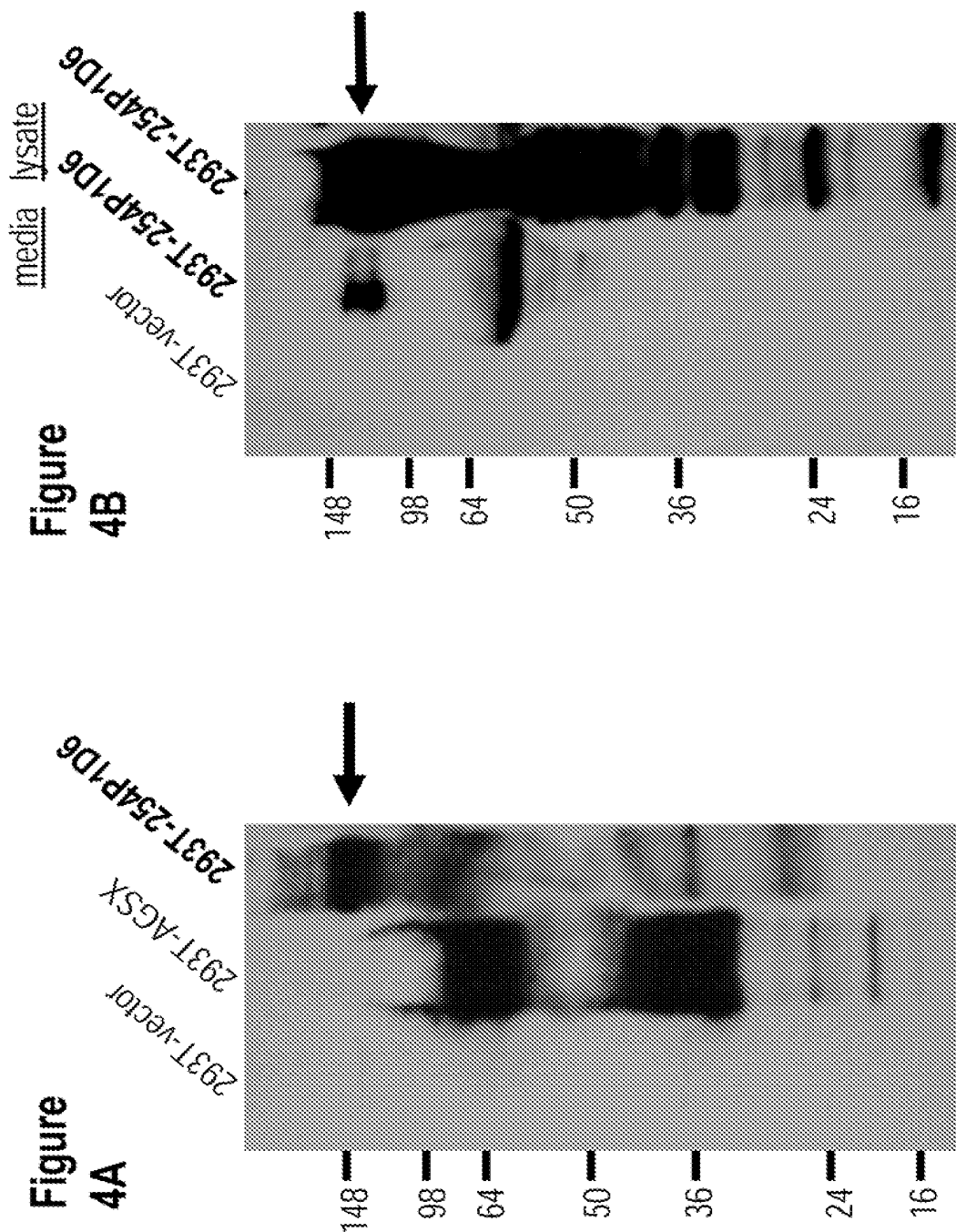


Figure 5: 254P1D6B variant 1
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

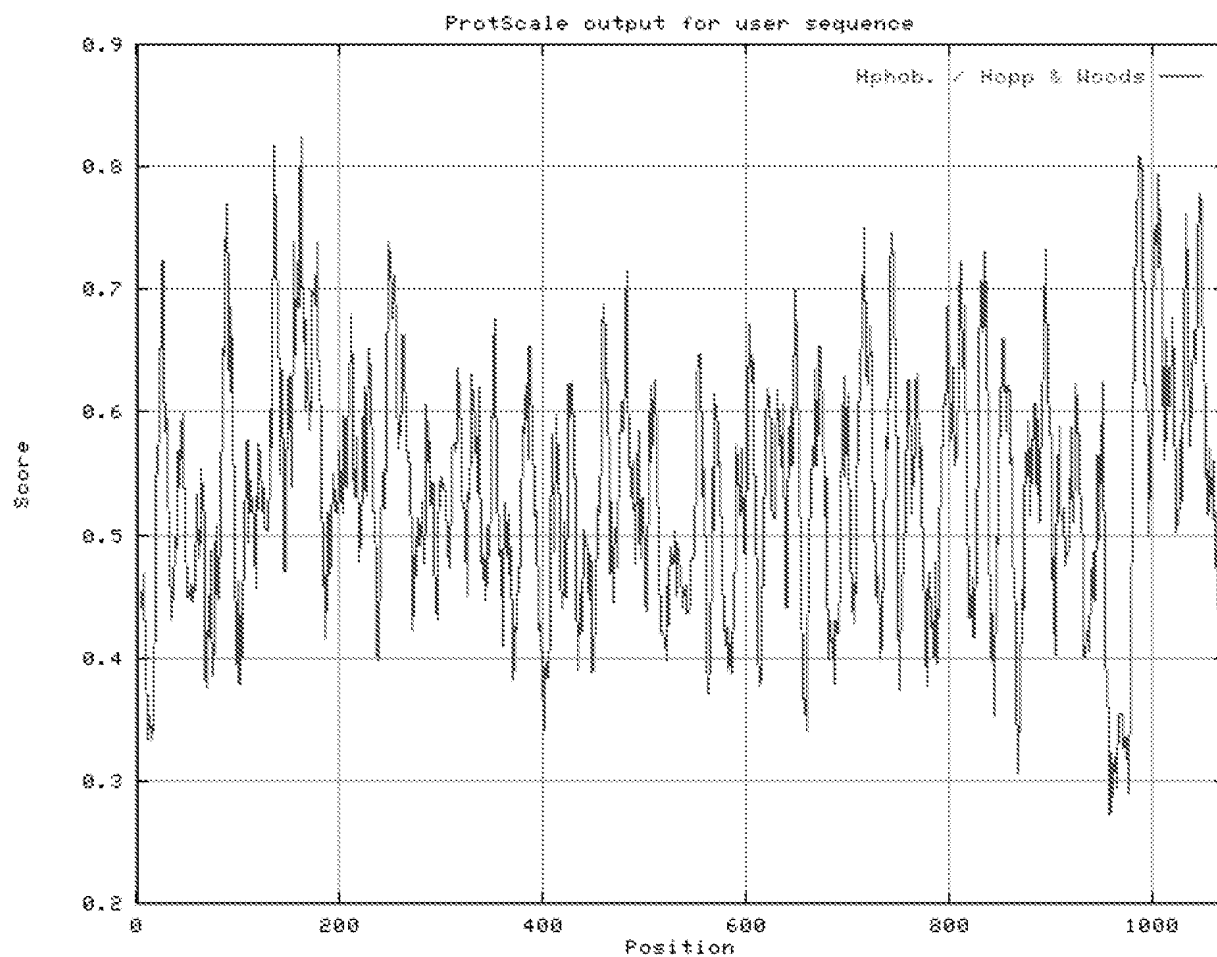


Figure 6: 254P1D6B variant 1
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

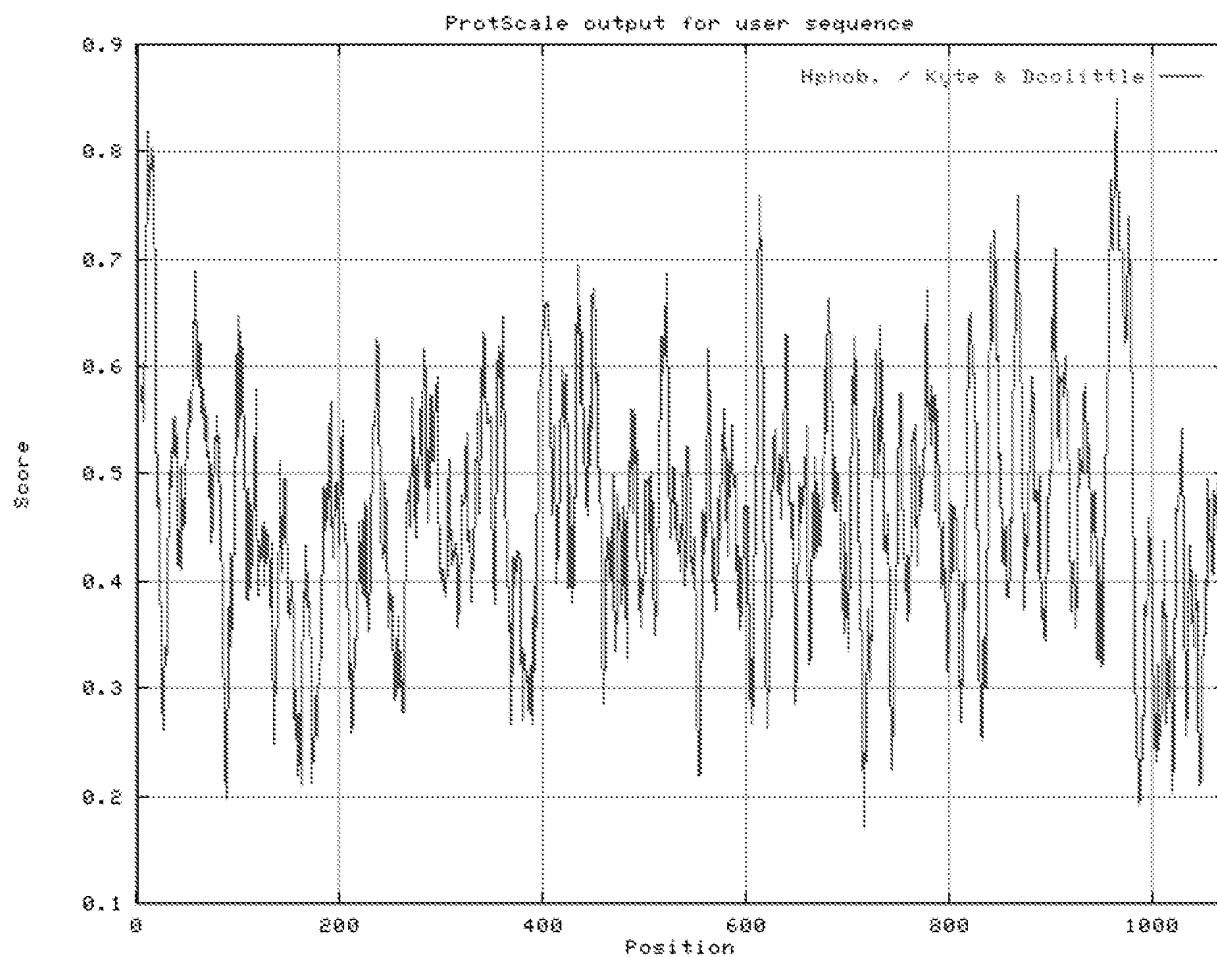


Figure 7: 254P1D6B variant 1
% Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

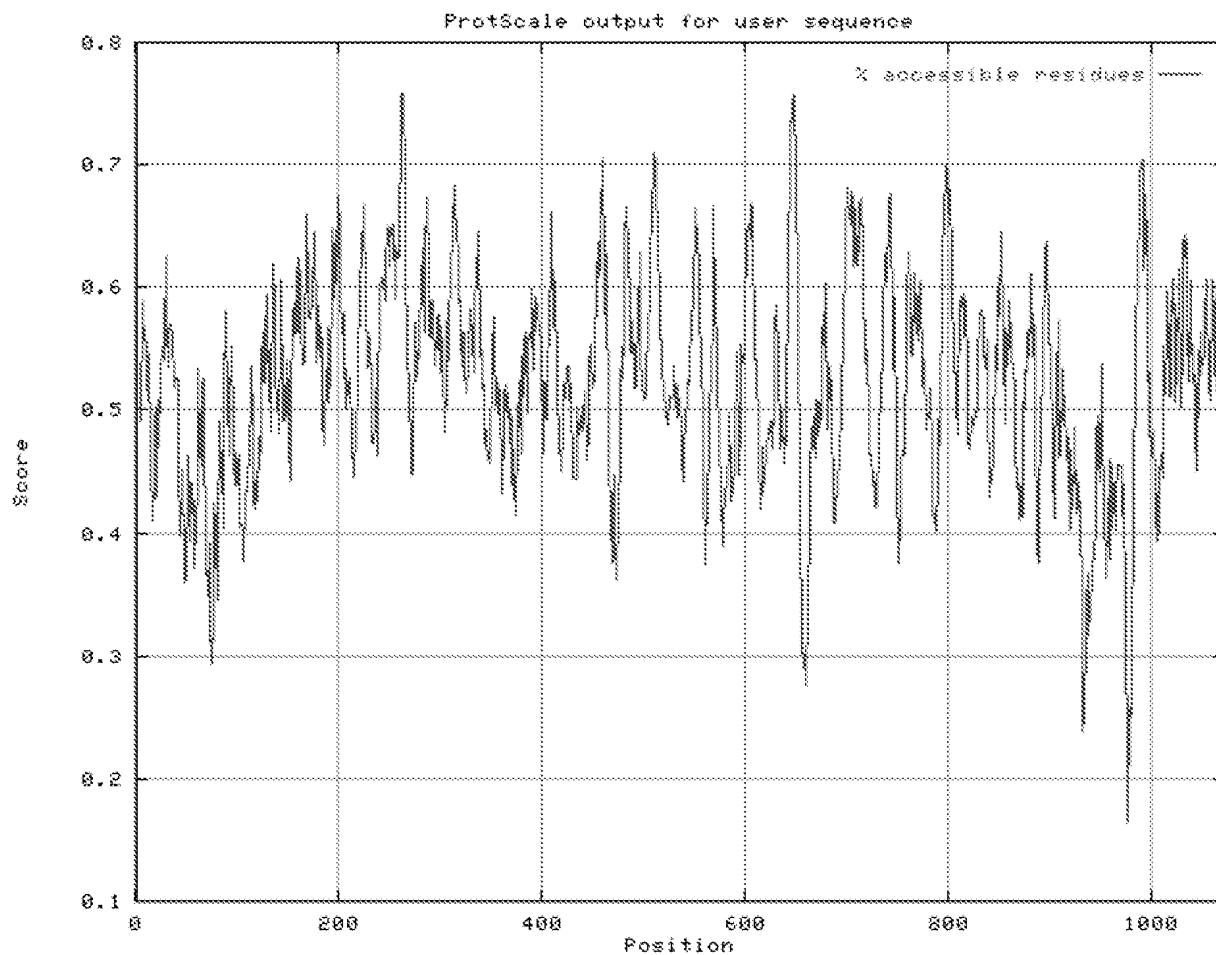


Figure 8: 254P1D6B variant 1
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

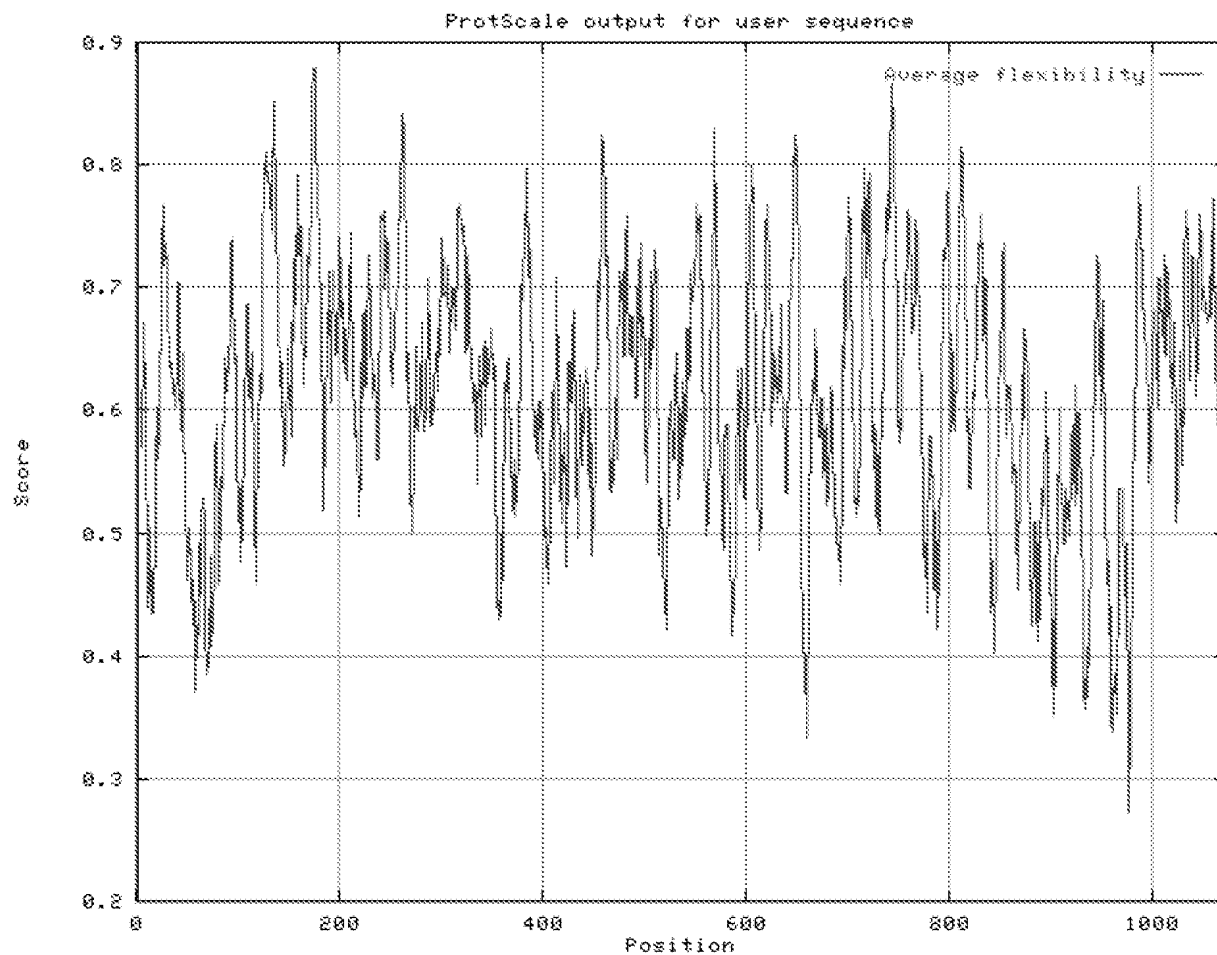


Figure 9: 254P1D6B variant 1
Beta-turn Profile
(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

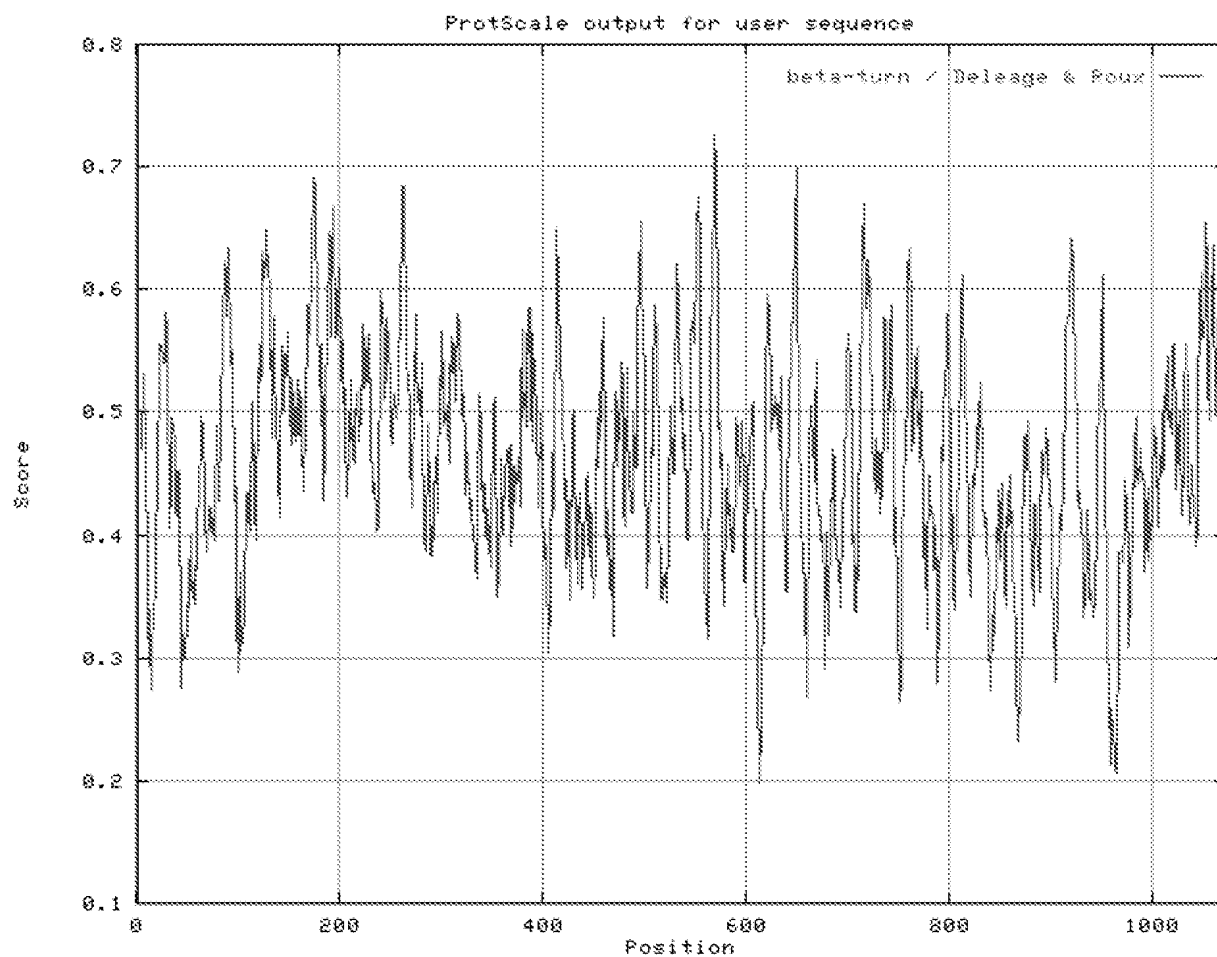


Figure 10

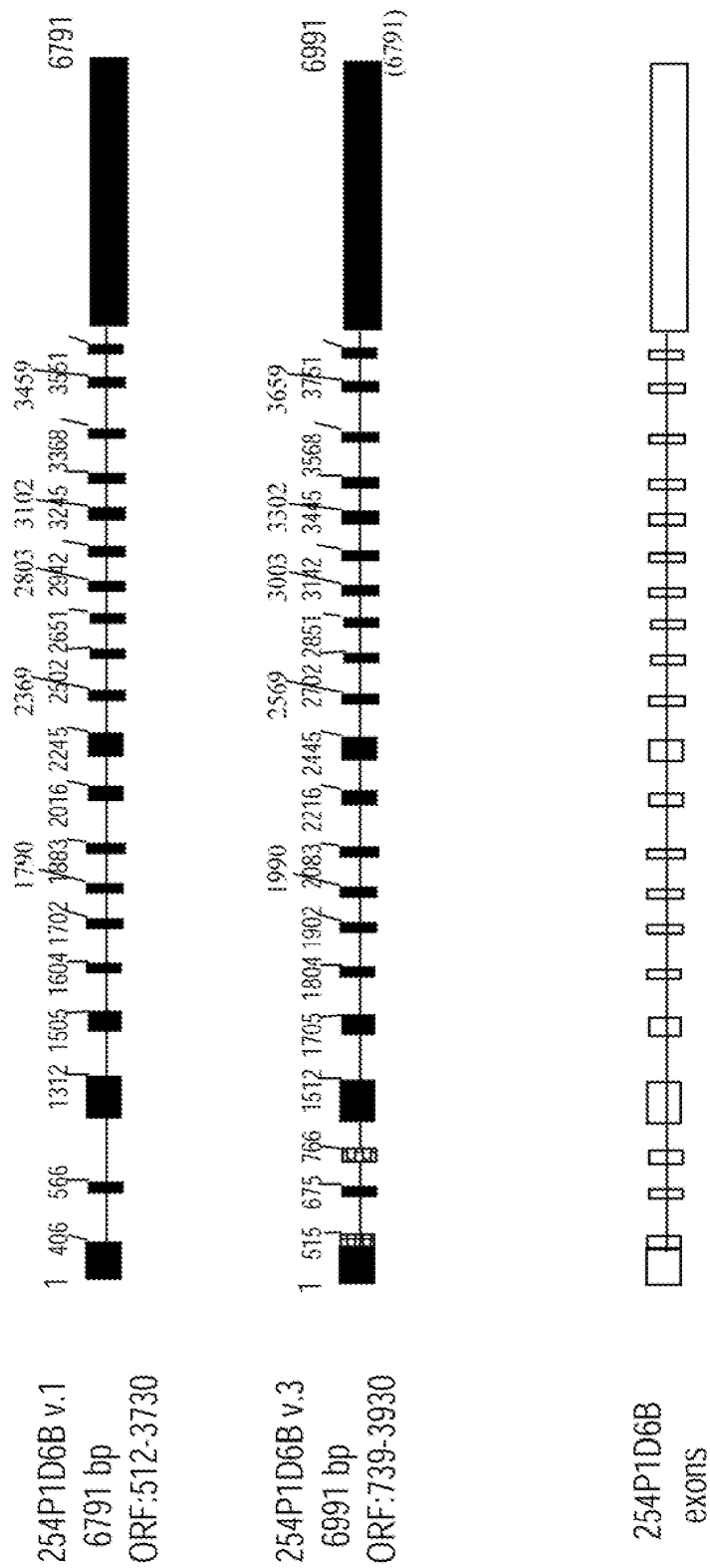


Figure 11

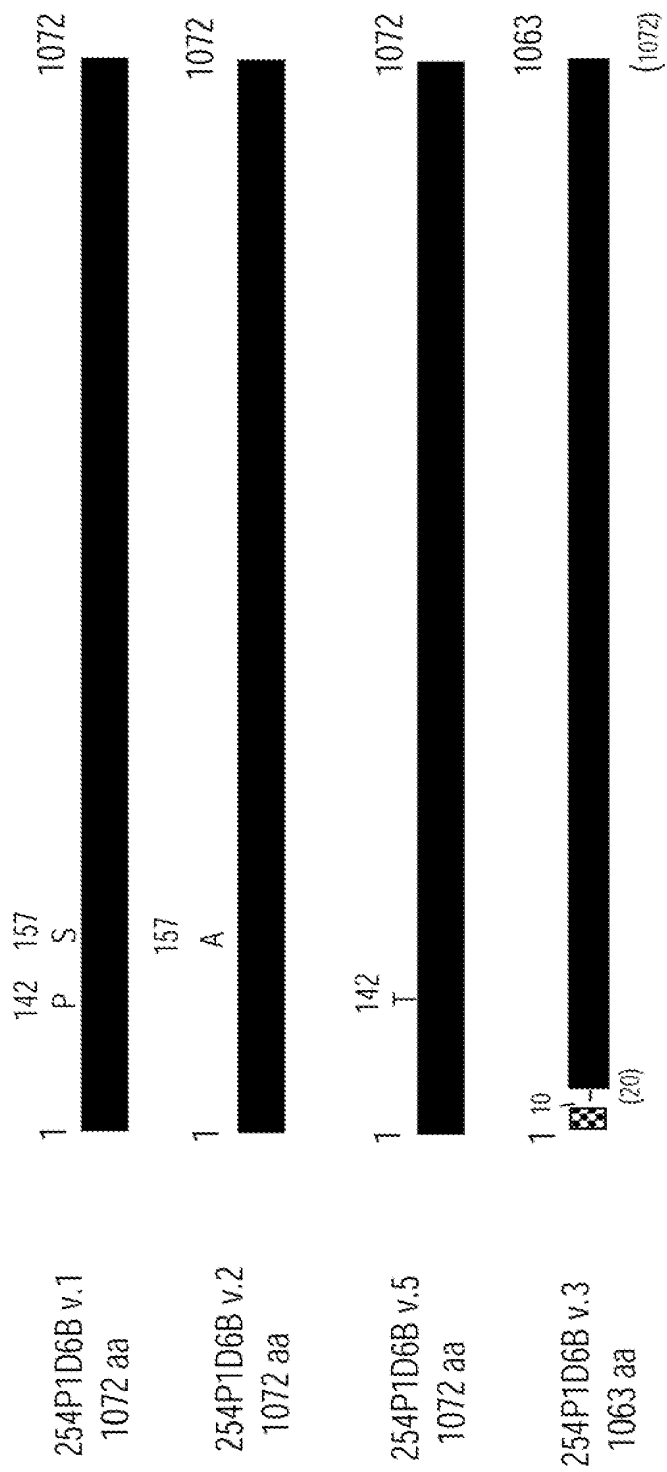


Figure 12

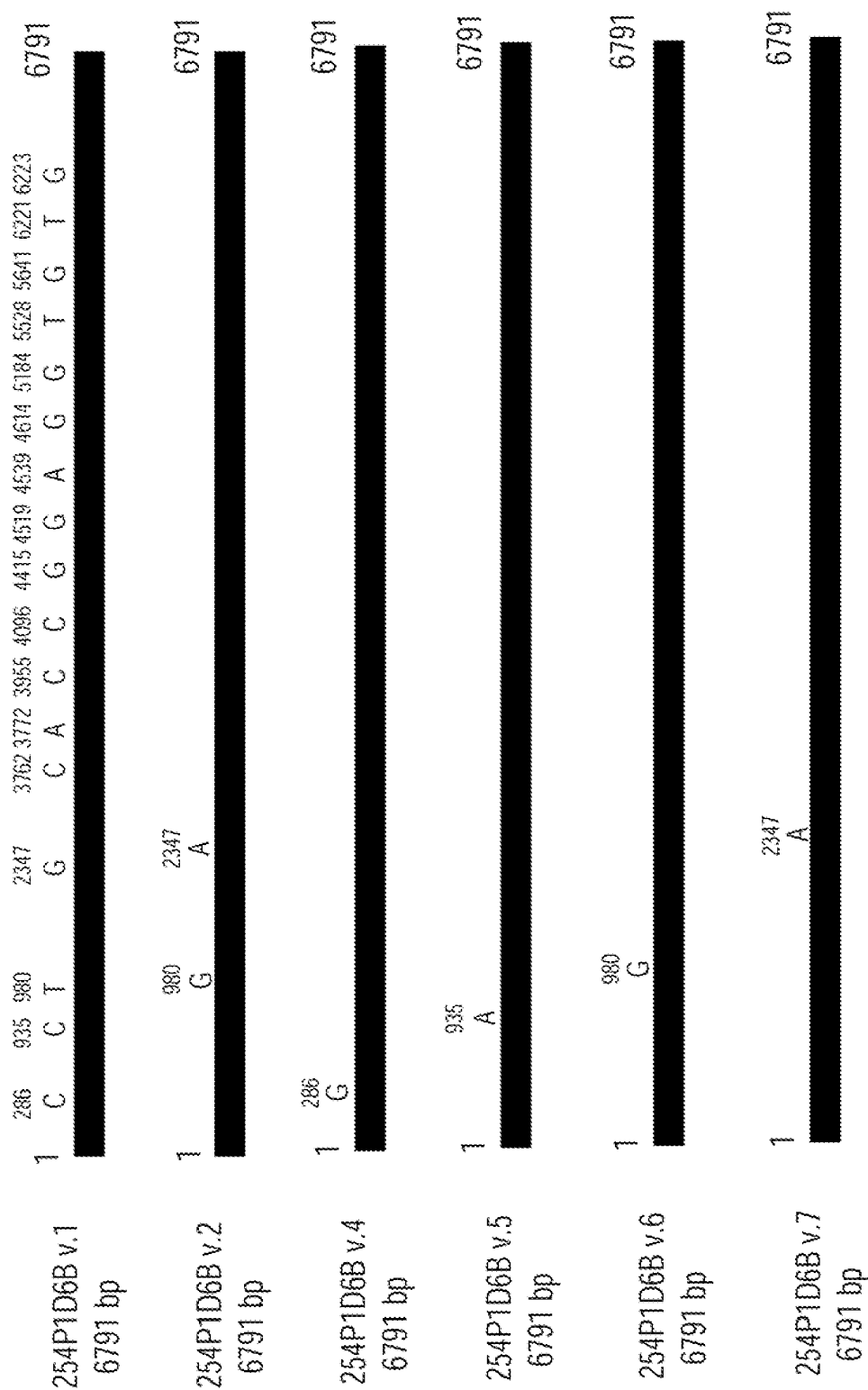


Figure 12-2

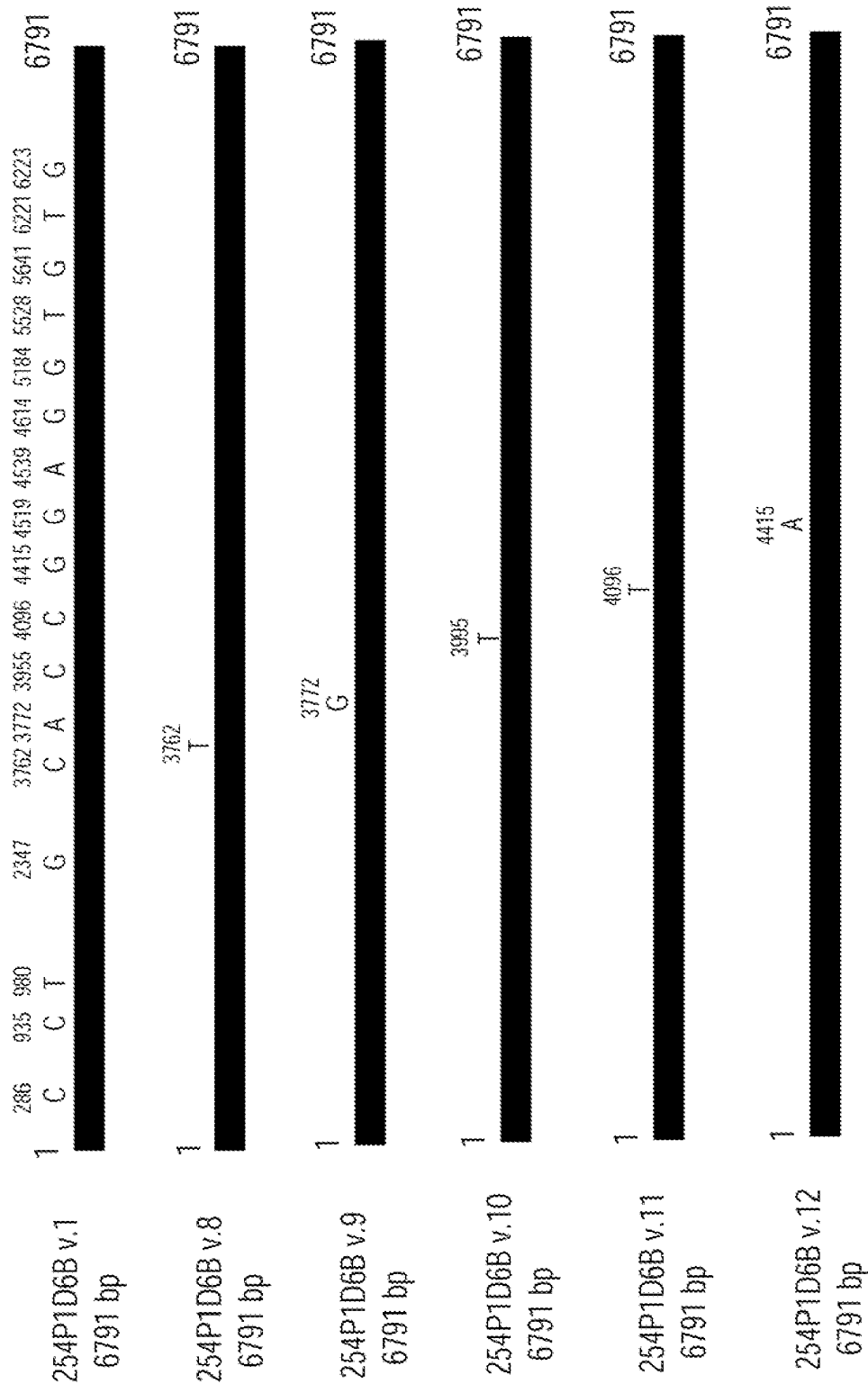


Figure 12-3

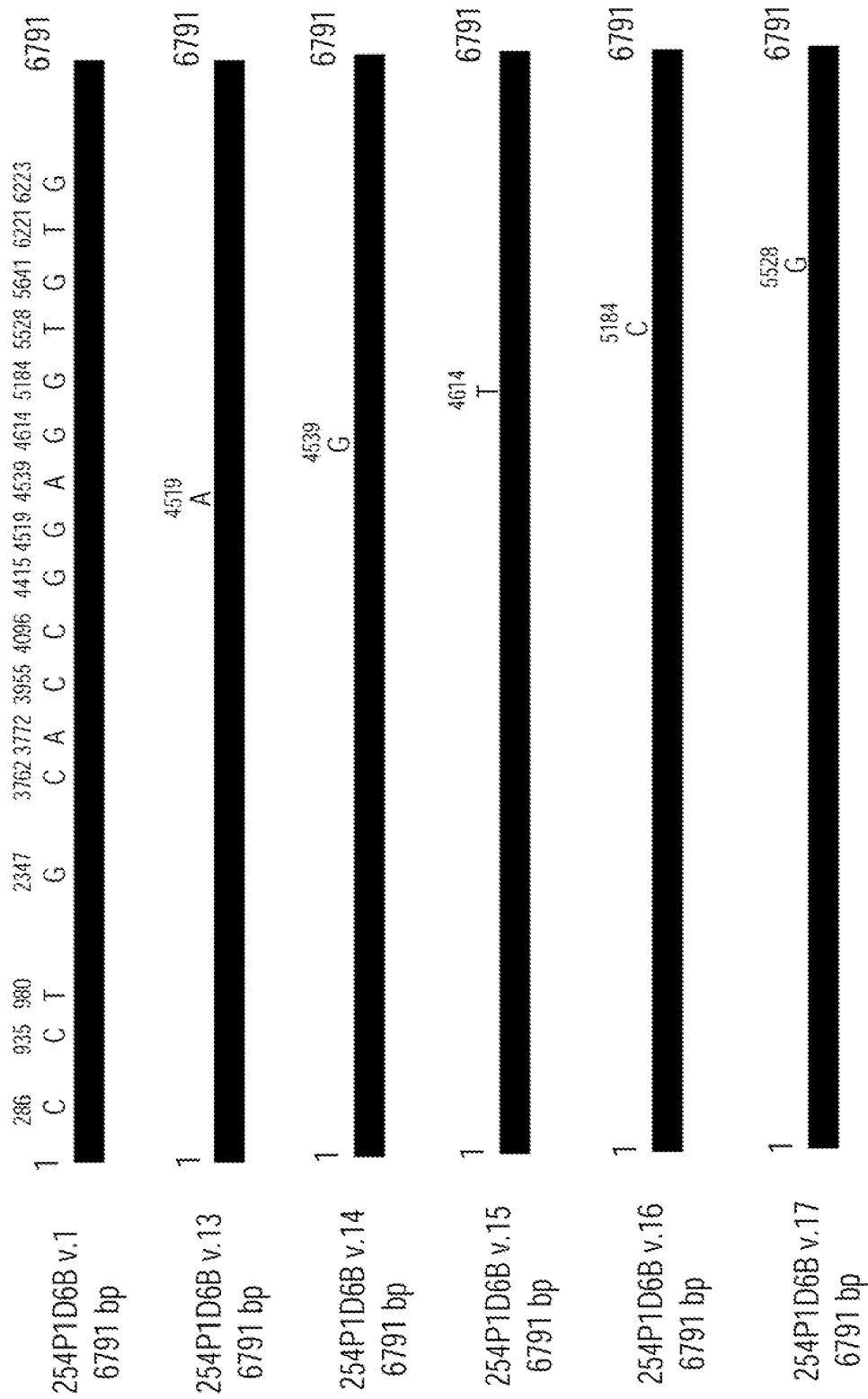


Figure 12-4

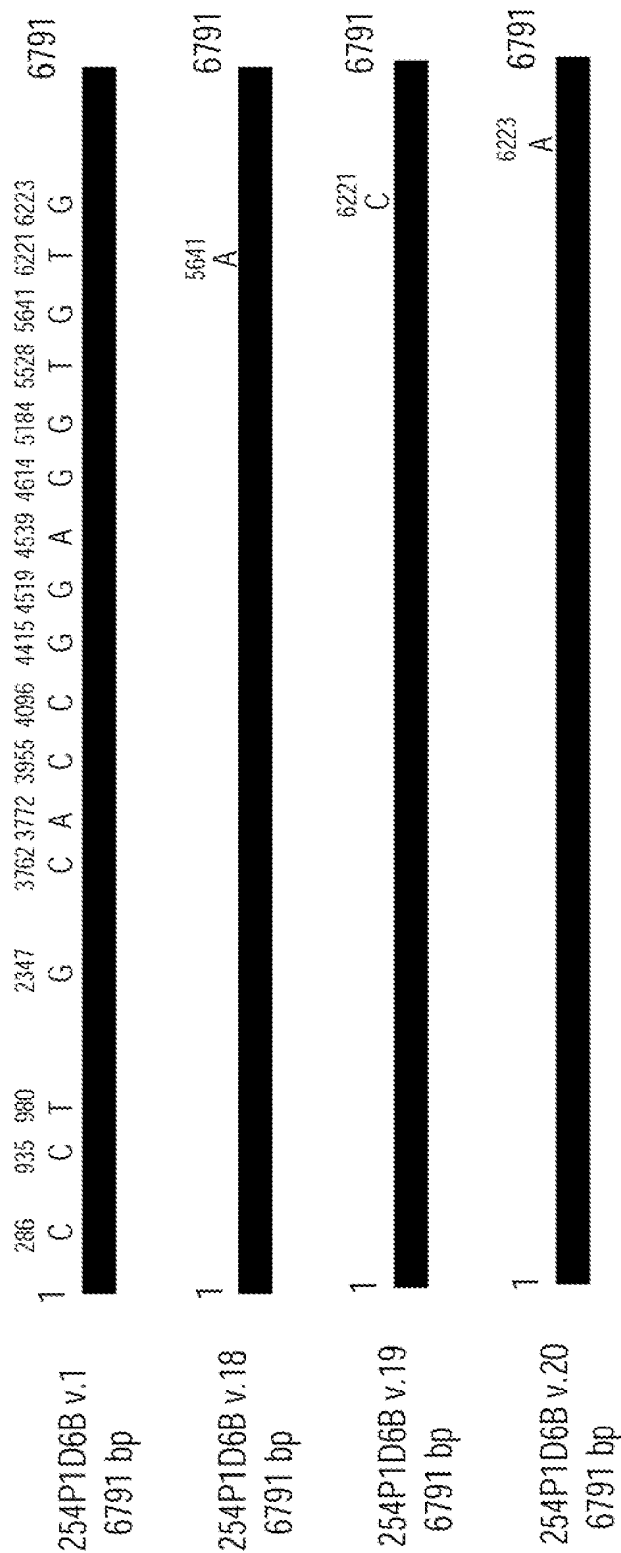


Figure 13A: Secondary structure prediction of 254P1D6B variant 1

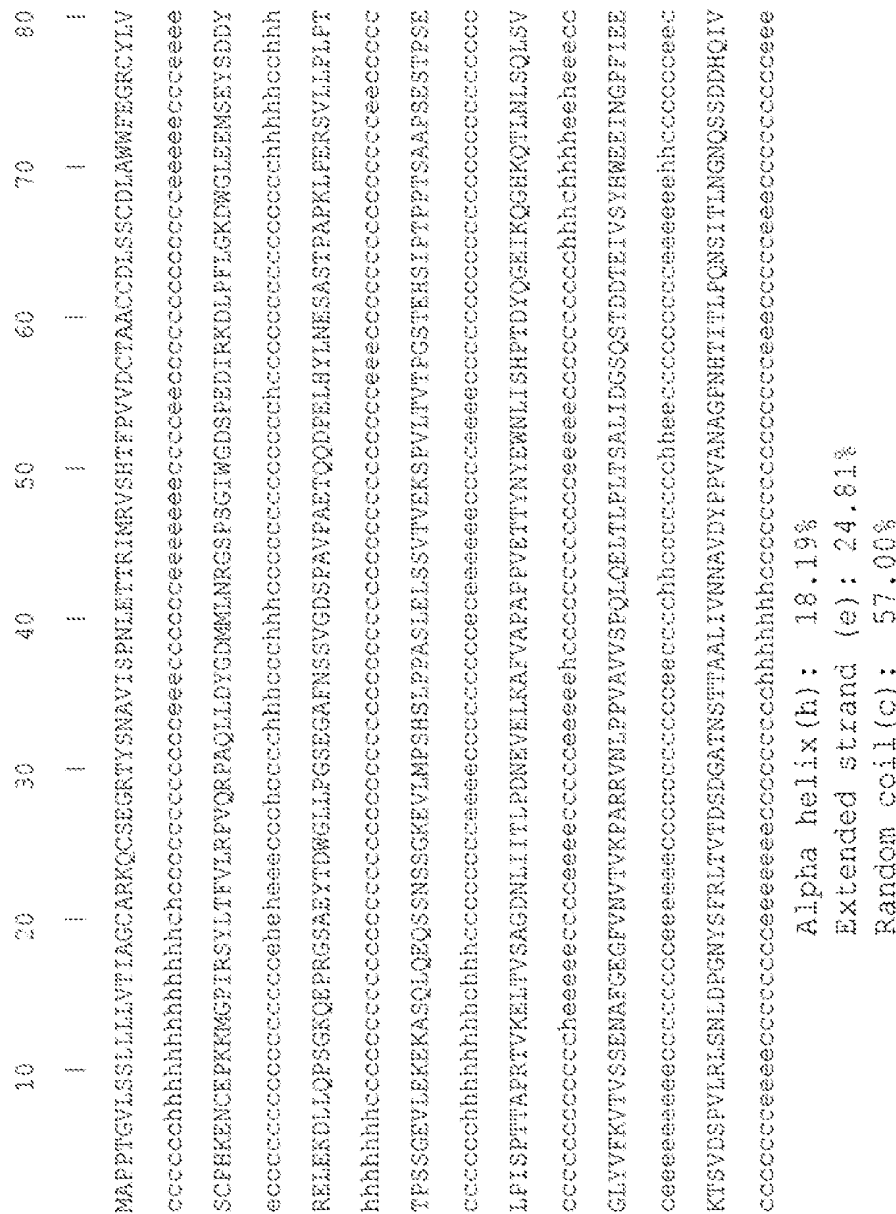


Figure 13A-2

```

570      580      590      600      610      620      630      640
|      |      |      |      |      |      |      |
LLENSLPGSECKHVMQGVCTFYHLSAMQEGDYTFQLKVTDSRQSTAVTVIVQFENNRPVAVAGFDKELIFVE
eeeecccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
SAILDGSSESDDHGIVFYHWEHVNGPSAVEMENIDKALATVTCLOVGYTHFRLTVKDDQGLSSTSTLTVAVKKNNSPPR
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLINRQSPAGDVIDGSDHSAIQLTNLVEGYTHLRLVTDSSQGASD
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
TDTATVEVQDPDKSGLVLELQVGVQLFEKORKNDILVPLQAVLLNVLDSDIKVQIRAHSDLSTVIVTVQSRPPFKVL
cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
KAEVARNLHMRLSKEKADLLEFKVLRVDTAGCLLKCSGCHCDPLTKRCICSHLWENLIQRYIWDGSENCENSIFYVT
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
VLAFTLLVLTGGFTWLCICCKRQKRTKIRNKTXYTILDNWDQERMELRPKYGIKRSSTEHNSSLMVSESEFDSTQDTI
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
FSREKMERGNPKVSMNGSIRNGASFSYCSKDR
ehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

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Alpha helix(h): 18.19%
 Extended strand (e): 24.81%
 Random coil(c): 57.00%

Figure 13B: Transmembrane prediction for 254P1D6B variant 1

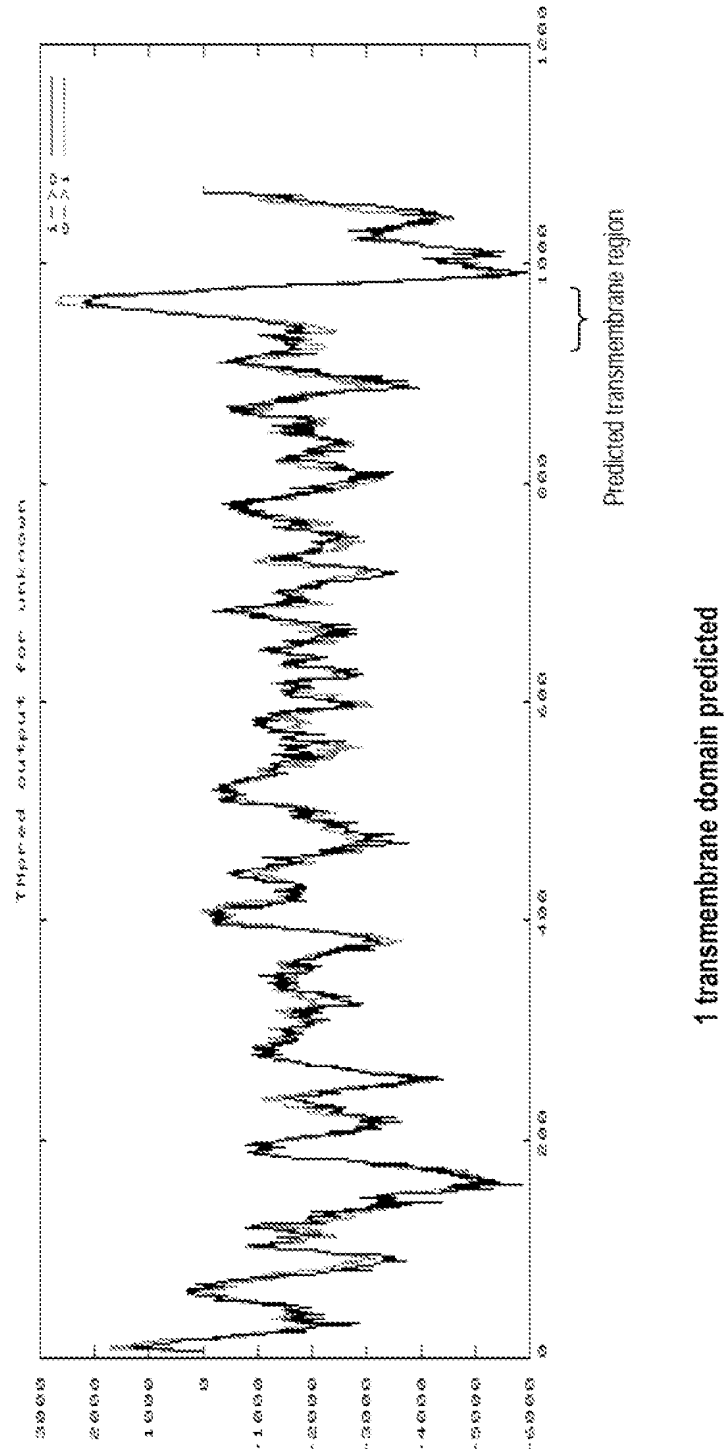


Figure 13C: Transmembrane prediction for 254P1D6B variant 1

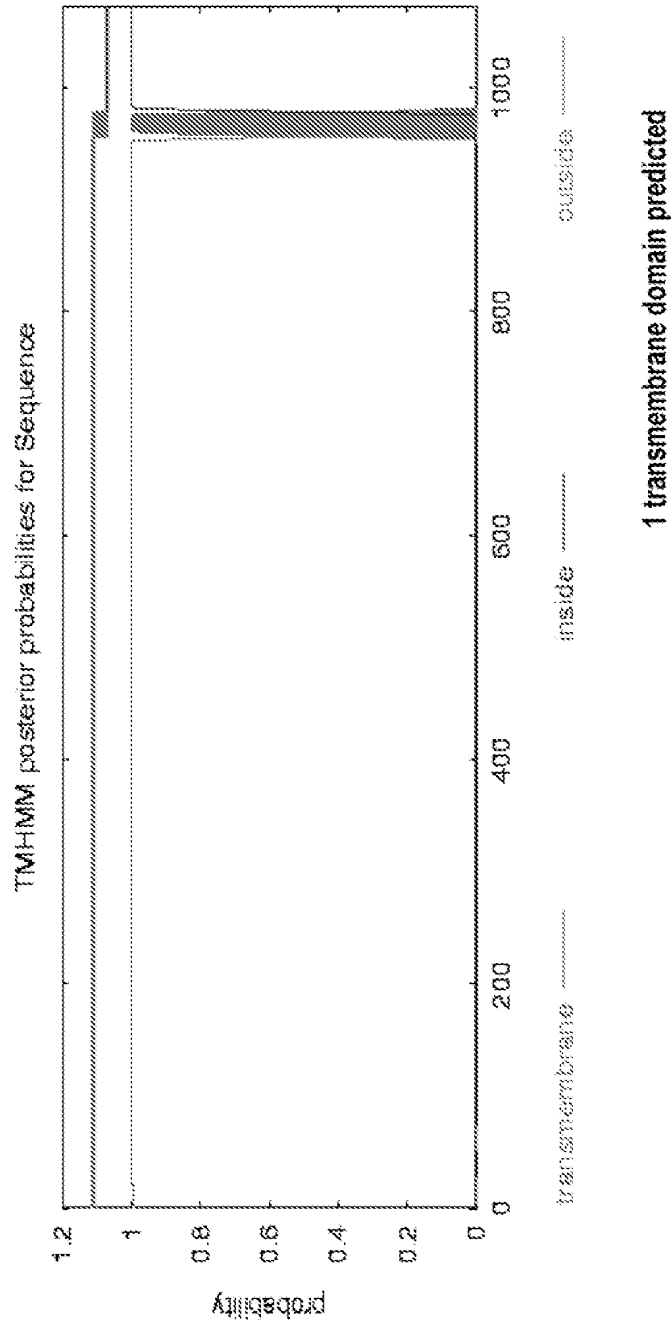


Figure 14A: 254P1D6B Expression by RT-PCR

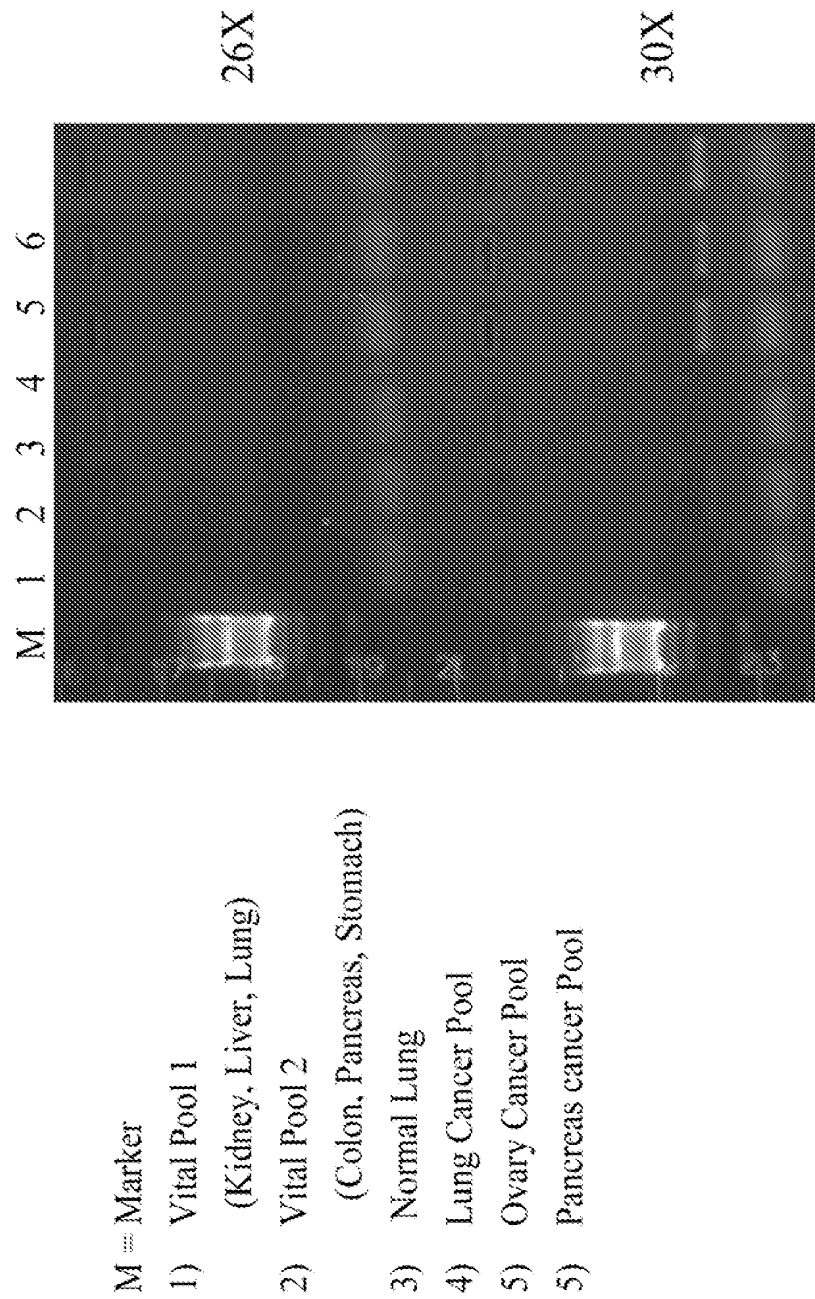


Figure 14B: Expression of 254P1D6B in Normal Human Tissues and Ovarian Cancer Patient Specimens

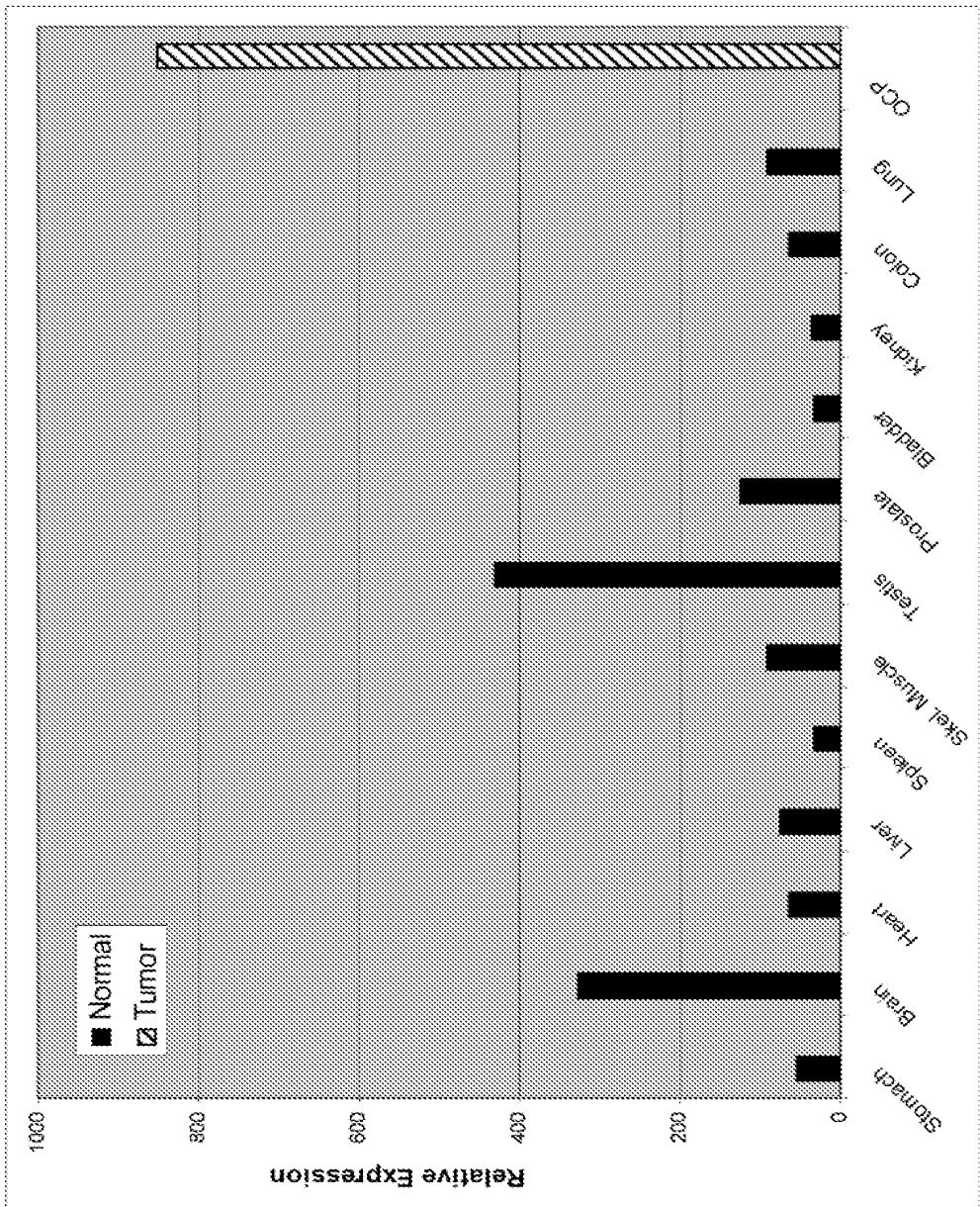


Figure 15: Expression of 254P1D6B in Normal Tissues

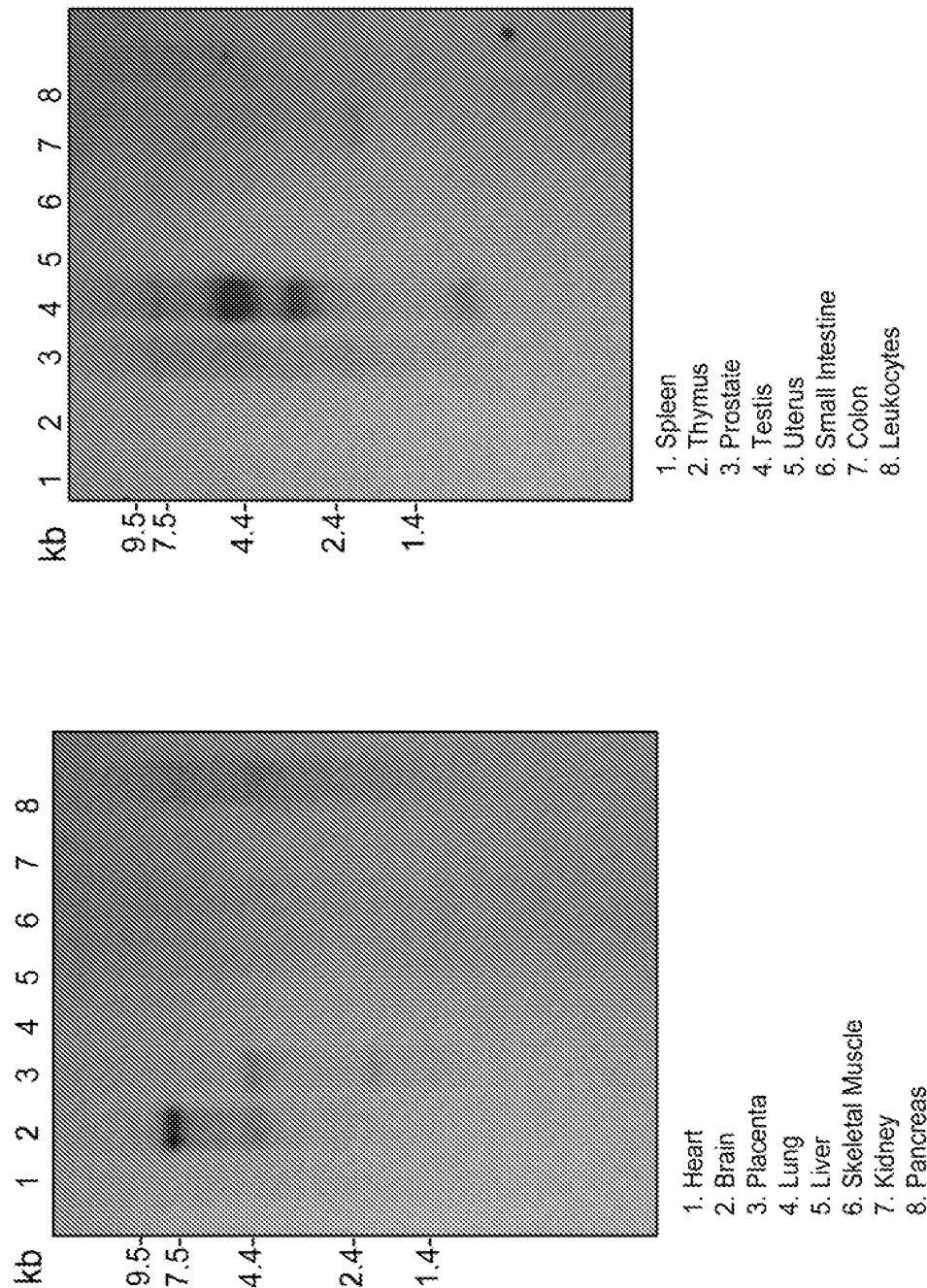


Figure 16: Expression of 254P1D6B in Lung Cancer Patient Specimens

